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- protein search, using sw model OM protein October Run on:

6, 2004, 15:50:37 ; Search time 123 Seconds (without alignments) 399.701 Million cell updates/sec

US-10-009-792C-19 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003bs:* geneseqp2003bs:* A_Geneseq_29Jan04:* 40070 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

uo	G-CSF ded	G-colony	Granulocy	Human G-C	Human CSF	Human G-C	Granulocy	Human gra	Mature gr	Human hG-		Codon opt	Human G-C	Human wil	Human gra	Wild-type	Human gra	Human gra	Human gra	Partial h	Human gra	Human pro	Human gra	Human gra	00000000
Description	Aap80965	Aap90470	Aar13679	Aar26909	Aar34707	Aaw02204	Aay78937	Aab14850	Aay97016	Aae12153	Aab61930	Aab85332	Aam52110	Aae11983	Aau79877	Aau97116	Aae14694	Abr55839	Aae30598	Abg74368	8	Adc56722		Abr61549	0001500
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Carrendo OI	AAP80965	AAP90470	AAR13679		AAR34707	AAW02204	AAY78937	AAB14850	AAY97016	AAE12153	AAB61930	AAB85332	AAM52110	AAE11983	AAU79877	AAU97116	AAE14694	ABR55839	AAE30598	ABG74368	ABR62687	ADC56722	ABR61548	ABR61549	4
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ALIGNMENTS

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The sequence of the gene is carried on plasmid pCSF1-2 isolated from a CDNA library prepared from mRNA extracted from peripheral blood macrophages. The deduced protein sequence agrees with those determined for G-CSF from the human squamous cell line CHU-II and the human bladder cancer cell line 5637. The DNA can be used as a "master agne" for the construction of mutant genes which encode variants of hG-CSF which differ by at least one AA. See also AAP80963 and AAP80964, and AAP82874-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human granulocyte colony stimulating factor polypeptide derivs. - \hbar \epsilon at least one different aminoacid, giving high specific activity and
                                                                                                               G-CSF deduced from gene isolate from peripheral blood macrophages.
                                                                                                                                                                                                                                                                                                                                                                      Sato M, Okabe M, Morimoto M;
                                                                                                                                          Granulocyte colony stimulating factor; hG-CSF; macrophage; tumour therapy; leukaemia.
                            AAP80965 standard; protein; 174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page ?; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Miyaji H,
                                                                                                                                                                                                                                                                                 87EP-00119157.
                                                                                                                                                                                                                                                                                                             86JP-00306799.
                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Kuga T, Komatsu Y,
Itoh S, Yamasaki M;
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1988-176825/26.
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                                                                                                                                                                                         Homo sapiens.
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                                                        AAP80965;
RESULT 1
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having

Query Match

100.0%; Score 896; DB 1; Length 174;

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LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide prodn. by fermenting transformed host cells - in presence non-auxotrophic aminoacid to increase prod. accumulation, esp. for granulocyte colony stimulating factor.
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        MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
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                                                                                                                                                                     Granulocyte colony stimulating factor.
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                                                                         AAR13679 standard; protein; 174
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91GB-00004126.
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                                                                                                                                                                                             G-CSF; neutropaenia.
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Best Local Similarity
Matches 174; Conserv
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13-NOV-1991
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AAR26909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New lysine depleted variants of polypeptide - opt. modified with hydrophilic residues, biologically active but with altered solubility,
                                                                  TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
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                       Indels
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           Pred. No. 3.8e-90;
Mismatches 0;
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100.0%; Pred. No. 3.8e-90;
iive 0; Mismatches 0;
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100.0%; Pre
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(first entry)
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                      174; Conservative
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N-PSDB; AAN90256.
           Best Local Similarity
Matches 174; Conserv
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Best Local Similarity
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                                                                                                                      Homo sapiens.
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Best Local Simi]
Matches 174; (
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                                                    Human CSF
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 AAR34707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is encoded by the synthetic gene AAQ28371. The plasmid containing the coding gene contains a novel inducible selection gene which is only expressed during the construction and testing phases of genetic manipulation. When the subsequent plasmid carrying the cloned gene is stably maintained in its bacterial host, the need for selection ceases. Cultures grown to express the cloned gene prod. will not require addn. of the selection drug and will not express the prod. of the selection gene. In this case the product of the cloned gene is human G-CSF which is used to treat neuropaenia associated with chemotherapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              radiation therapy, or autologous bone marrow transplantation, to stimulate bone marrow suppression associated with AIDS, in the treatment of myelodysplastic syndromes characterised by gramulocyte functional abnormalities and as an adjunct to the treatment of severe infections. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                G-CSF; granulocyte colony stimulating factor; inducible selection; ricin A; lummunotoxins; neutropeantia; chemotherapy; radiation; therapy; autologous bone marrow transplantation; AIDS; severe infection; myelodysplastic syndromes; abnormal granulocyte function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Fig 10; 73pp; English.
                                                                                                                                                                                                                                                                                   IMPERIAL CHEM IND PLC.
                                                                                                                                                                                                                 92EP-00301465
                                                                                                                                                                                                                                           91GB-00004017.
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 25-MAR-2003
20-MAY-1998
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                                       Human G-CSF
                                                                                                                                   Synthetic.
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The sequence is that of human colony stimulating factor, which can be with an immunotherapeutic agent for cancer and an anticancer fung in a novel anticancer compsn. The compsn. has excellent anticancer effects, not shown by sole administration of the single components. It shows good life prolonging effects and has tumour growth inhibiting effects for mammalian cancers. It is esp. effective for treatment of early stage cancer and after cancer surgery. Treatable diseases include various kinds of sarcona, malignant lymphoma, malignant melanoma, malignant chlorionic tumour, phalia cancer, various kinds of digestive organ cancer, lung cancer, etc. See also AAR32258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LSSCPSQALQLAGGLSQLHSGLFLYQGLLGALEGISPELGPTLDTLQLDVADFATTIWQQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     good apothanaisia effect - contains for cancer, human colony stimulating factor and
Colony stimulating factor; cancer; tumour; sarcoma; lymphoma; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 MEELGMAPALOPTOGAMPAFASAFORRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
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0
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                                                                                                                                                                                                                                                                                                                                   90JP-00246488
90JP-00287707
                                                                                                                                                                                                                                                                                                                                                                                                                          (CHUS ) CHUGAI PHARM CO LTD
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This sequence represents a human granulocyte colony-stimulating factor-CSF) polypeptide. G-CSF is used in a powder preparation which is administered via the mucus membrane. The preparation comprises a polymeric medicine and a cationic polymer. The preparation is used for the mucosal administration of polymeric pharmaceuticals and has good absorption through the mucous membrane and improved bloavailability
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                                                                                                                                                                                                                                                                                                                                                                     LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A non-naturally occurring granulopoietic activity protein (GPA) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, granulocyte colony stimulating factor; G-CSF; neutropaenia; bone marrow suppression; infection.
                                                                                                                                Powder preparation for mucosal administration of polymeric drug, peptide, protein, antibody, vaccine or antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                            Length 174;
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                            Score 896; DB 3;
Pred. No. 3.8e-90;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human granulocyte colony stimulating factor #1.
                                                                                                                                                                           Disclosure; Page 39-40; 45pp; Japanese
                                                                                                                                                                                                                                                                                                                             100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB14850 standard; protein; 174
           98JP-00192722.
99JP-00081549.
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99US-0118831P.
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 174; Conservative
                                                   (KIRI ) KIRIN AMGEN INC.
                                                                                                         WPI; 2000-182173/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-465988/40.
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                                                                                                                                                                                                                                                                                                     Sequence 174 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200040728-A1.
           08-JUL-1998;
25-MAR-1999;
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05-FEB-1999;
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                                                                                Nomura
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AAB14850
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                                                                                                                                                                                                                                                                                                               An agent contg, human interleukin 11 (hIL-11), and pref. human granulocyte colony stimulating factor (hG-CSF), i.e. the present protein, can be administered in vivo to increase the prodn. of human peripheral blood (hPBS) cells. The agent may further exprise hIL-1, hIL-3, stem cell factor, leukaemia inhibitory factor, erythropoietin, GM-CSF and M-CSF, which synergistically increase hPBS cell prodn. The amt. of hIL-11 or hIL-11 plus hG-CSF is generally 0.001-100, preff 0.1-10 wt. %. The agent may contain a stabiliser (e.g. serum albumin) and fillers (mannitol). The dose is 0.1-1000 microg/kg/day, and the agent can be used in hPBS cell transplants for the treatment of blood system diseases
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                                                                                                                                                                                                                                Agent contg. human interleukin 11 for increasing peripheral blood stem cell prodn. - pref. comprises human G-CSF, and is useful for peripheral blood stem cell transplants to treat blood system diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174
'GM-CSF; M-CSF; transplant; treatment; transfusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colony-stimulation factor (G-CSF) peptide sequence #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Granulocyte colony-stimulating factor; G-CSF; powder preparation; polymeric drug administration; mucus membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 896; DB 2;
100.0%; Pred. No. 3.8e-90;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                         Example 1; Page 6; 6pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein; 174
                                                                                                                         94JP-00266826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 174; Conservative
erythropoietin; GM-CS
blood system disease.
                                                                                                                                                                              (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                        WPI; 1996-295521/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200002574-A1
                                         Homo sapiens
                                                                   JP08127539-A
                                                                                                                         31-OCT-1994;
                                                                                                                                                   31-OCT-1994;
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                                                                                               21-MAY-1996
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(G-CSF)-responsive disease identical to hG-CSF.
                                                                                            colony stimulating factor (G-CSF). This protein is involved in the profile profile are and differentiation of gramulocytes in the blood. The sequence was used to create the proteins of the invention, which are designated gramulopoietic activity (GPA) proteins. These can be used instead of G-CSF, which has a short half-life in the blood and is unstable in storage, in treatments for neutropaenia associated with cancer therapies, radiation accidents, bone marrow transplantation, bone marrow suppression conditions such as ALDS, myelodysplastic syndromes characterised by granulocyte functional abnormalities, and severe infections. They can also be used to enhance peripheral blood progenitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pharmaceutical composition for the sustained-release of a biologically active agent (BAA), such as granulocyte-colony stimulating factor, comprises incorporating the BAA into a biocompatible polyol/oil
                                                                                 The present sequence is the protein sequence for the human granulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                            TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIEWAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-CSF; granulocyte colony stimulating factor; sustained-release; biocompatible polyol/oil suspension; anti-inflammatory.
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                                                                                                                                                                                                                                                                                                                                     Length 174;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                 ; Score 896; DB 3;
; Pred. No. 3.8e-90;
0; Mismatches 0;
treating granulocyte colony stimulating factor comprises an amino acid sequence less than 95%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocyte colony stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beekman AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY97016 standard; protein; 174 AA
                                                 Disclosure, Fig 1, 63pp, English.
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99US-00448205.
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                                                                                                                                                                                                                                                                                                                                                                       Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                     Sequence 174 AA;
                                                                                                                                                                                                                                                                     cell collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-1999;
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A pharmaceutical composition comprising a biologically active agent (BAA) incorporated into a biocompatible polyol/oil suspension which contains a thickener is new. The compositions are used for the sustained-release of a BAA such as an incerferon consensus, EPO, granulocyte-colony stimulating factor, stem cell factor, leptin, tumor necrosis factor-binding protein, interleukin-1 receptor antagonist, brain derived neurotrophic factor, glial derived neurotrophic factor, metrophic factor, glial derived neurotrophic factor, neutrophic factor, stemprotegerin, granulocyte macrophage colony stimulating factor, thrombopoletin, or novel erythropoises; stimulating protein (claimed). The release of a medicament can be controlled to provide longer periods of consistent release that previous methods of treatment do not achieve, such as repeated injections. Blood levels of the active ingredient can be controlled, providing an enhanced prophylactic, therapeutic, or diagnostic effect as well as greater safety, patient convenience and patient compliance. The compositions can lead to dose sparing and a lower cost, in protection,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPLGPASSIPOSFILKCLEQVRKIQGDGAALQEKICATYKLCHPEBIVLLGHSIGIPWAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, granulocyte colony stimulating factor, hG-CSF; protease, Factor Xa, kanamycin resistance, endoxylanase signal peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 174;
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                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 896; DB 3;
100.0%; Pred. No. 3.8e-90;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                stability and potency are increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE12153 standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 174; Conservative 0
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N-PSDB; AAD19771.
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 174 AA;
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RESULT 12
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                            The invention relates to an Escherichia coli producing and secreting human granulocyte colony stimulating factor (NG-CSF), more specifically, to a recombinant plasmid constructed to express secretory MG-CSF in E. coli, an E. coli transformed with that plasmid to secrete hG-CSF, and a process for preparing hG-CSF using the transformed hG-CSF. The combinant plasmid vector comprises of a kananycin resistance gene, a promoter, an endoxylanase signal sequence, a nucleotide sequence coding for an oliopeptide consisting of 13 amino acids including 6 consecutive histidine residues and a hG-CSF. E.coli transformed with recombinant plasmid vector is useful for preparing hG-CSF. The method comprises culturing the microorganism to obtain a hG-CSF fusion protein and treating the fusion protein with a protease preferably Factor Xa, to obtain a hG-CSF, where the fusion protein is obtained from the culture by employing Ni-column. The present sequence is human hG-CSF inserted into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Granulocyte-colony stimulating factor; G-CSF; human; variant.
                                                                                                                                                                                                                                Length 174;
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                                                                                                                                                                                                                                100.0%; Score 896; DB 4;
.larity 100.0%; Pred. No. 3.8e-90;
Conservative 0; Mismatches 0;
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          Example 1; Fig 3; 50pp; English
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Best Local Similarity
Matches 174; Conserv
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                                                                                                                                                                                                            Sequence 174 AA;
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AAB61930
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                                                                        Modified human granulocyte-colony stimulating factor (hG-CSF), retaining the biological activity of wild type hG-CSF, comprises replacement amino acids at the first, second, third and seventeenth positions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 174;
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Pred. No. 3.8e-90;
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100.0%; Pred. No. 5...
0; Mismatches
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                                                                                                                                                                                 Claim 1; Fig 1; 69pp; English.
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02-MAR-2000; 2000DK-0000341.
16-JUN-2000; 2000DK-00000943.
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WPI; 2001-138357/14.
N-PSDB; AAF56684.
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N-PSDB; AAH22902.
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Best Local Similarity
Matches 174; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 174 AA;
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Nomura

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The invention provides a polypeptide (PP) conjugate (I) exhibiting granulocyte-colony stimulating factor (G-CSF) activity, comprising PP with a maino acid (as) sequence that differs from as sequence of human G-CSF by at least one as residue comprising an attachment group for a non-PP group bound to attachment of PP, and the PP group and having a non-PP group bound to attachment of PP, and the C-CSF by a trivity. (II) and (II) are useful for treating general hemotopoietic disorders, including care useful for therapeutic, disquestic disorders, including cidesorders arising from radiation therapy or from chemotherapy, AIDS or immunodeficiency diseases, leukopenia and bacterial or other infections. (II) is useful for therapeutic, disquestic and other purposes and in particular finds use as intermediate products for preparation of (I). (I) cand (II) are used for preventing infection in cancer patients undergoing radiation therapy, chemotherapy and bone marrow transplantations, to combilize progenitor calls for collection in peripheral blood progenitor cell transplantations and to support treatment of patients with acute myeloid leukemia. A nucleofies sequence encoding (II) is useful in gene therapy applications. (I) has increased functional in vivo half-life, increased serum half-life, reduced renal clearance, reduced receptor mediated clearance, reduced side effects, such as bone pain, reduced immunogenicity and/or increased bioavailability. The present sequence represents a mature hG-CSF with cooperation of the expression in E. coll: This is used in the construction of synthetic genes encoding hG-CSF.
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activity and conjugates between the polypeptide and a non-polypeptide moiety, useful for treating leukopenia, AIDS and bacterial or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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100.0%; Pred. No. 3.8e-90;
ive 0; Mismatches 0;
                                                                                   Example 1; Page 91-92; 94pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KIRI ) KIRIN BEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 174 AA;
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                                          infections
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The invention relates to a stable powdered preparation for transmucosal administration (preferably nasally) comprising a polymentic form of drug (preferably peptides), a cationic polymer and at least one basic amino acid or its salt. The present sequence is that of human G-CSF polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                    LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ
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                                                        Stable powdered preparation for transmucosal administration comprises polymeric drug, cationic polymer and basic amino acid.
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100.0%; Score 896; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.8e-90;
Matches 174; Conservative 0; Mismatches 0;
                                                                                                      Disclosure; Page 23-24; 28pp; Japanese.
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20-MAR-2000; 2000US-0190844P.
25-AUG-2000; 2000WO-DK000471.
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                             WPI; 2001-662952/76.
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                                                                                                                                                                                                              Sequence 174 AA;
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25-AUG-2000;
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comprising at least one non-polypeptide moiety covalently attached to a polypeptide variant, wherein the amino acid sequence of the polypeptide variant that at least in corresponding wild-type human polypeptide in that at least I residue comprising an attachment group for the non-polypeptide group has been introduced and/or removed. The wild-type human polypeptide is selected from the group consisting of interferon-gamma (IFNG), interferon-beta, interferon alpha, follicle stimulating factor (G-CSP). The dispersion is used for the preparation of a medicament for pulmonary and/or circulatory administration. The present sequence is human wild type granulocyte colony stimulating factor (G-CSP)
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Matches 174; Conservative
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Human; granulocyte colony-stimulating factor, G-CSF; vasotropic; vulnerary; immunosuppressive; cerebroprotective; nephrotropic; respiratory; cardiant; antiartericosdlerotic; ischaemic disease; external wound; transplant rejection; ischaemic cerebrovascular descebral apoplexy; cerebral infarction; ischaemic kidney disease; ischaemic pulmonary disease; coronary occlusion; ischaemic limb disease; ischaemic heart disease; myocardial ischaemic limb disease; cardiac insufficiency; arteriosclerosis; kinesitherapy; pharmacotherapy; haemokinesis reconstruction; arteriosclerosis obliteran; gene therapy; Human granulocyte colony-stimulating factor (G-CSF). (first entry) 15-JUL-2002

AAU79877 standard; protein; 174 AA.

WO200222163-A1. Homo sapiens

intramuscular transplantation.

21-MAR-2002

13-SEP-2000; 2000JP-00277562.

13-SEP-2001; 2001WO-JP007946.

(CHUS) CHUGAI SEIYAKU KK.

Tamura M; Miyai T, WPI; 2002-371949/40.

Remedies for ischemic diseases comprise human granulocyte colony-stimulating factor.

Disclosure; Page 4-5; 21pp; Japanese

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The invention describes remedies comprising a human granulocyte colonystimulating factor (G-CSF). Used for treating and preventing ischemic diseases such as external wounds, transplant rejection, ischaemic cerebrovascular disorders (e.g. cerebral apoplexy and cerebral infarction), ischaemic kidney diseases, ischaemic pulmonary diseases, ischaemic pulmonary diseases, ischaemic infarction), tachaemic cerebral infarction), ischaemic kidney diseases, ischaemic limb diseases, ischaemic heart disease (e.g. myocardial ischaemid, myocardial infarction or cardiac insufficiency) or arteriosclerosis. Agents may also be used for overcoming problems occurring particularly in the conventional kinesitherapy, pharmacotherapy and haemokinesis reconstruction for arteriosclerosis obliterans, gene therapy and intramuscular transplantation. This is the amino acid sequence of the human granulocytic colony-stimulating factor (G-CSF)
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ZIP: Z005-3918
COMPUTER READALE FORM:
MEDIUW TTPEB. 144M diskette
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RElease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,459A
FILING DATE: 20-MAR-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/215,676
FILING DATE: 22-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,306
FILING DATE: 27-FEB-1991
PRIOR APPLICATION NUMBER: GB 9004390.2
FILING DATE: 27-FEB-1990
SPELICATION NUMBER: GB 9004390.2
FILING DATE: 27-FEB-1990
SELING DATE: 27-FEB-1990
SECURATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               Sequence 31, Application US/08431459A;
Sequence 31, Application US/08431459A;
Patent No. 5840543.
GENERAL INFORMATION:
APPLICANT: Kara, Bhuphendra V.
ITLE OF INVENTION: PERMENTATION PROCESS;
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: PILLSBUTK MADISON & SUTRO, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: DC
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Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0;
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TOPOLOGY: linear
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Sequence 5, Application US/08722258
; Patent No. 6011002
; GENERAL INFORMATION:
APPLICANT: Pateran, Ira
APPLICANT: Freitman, Robert J.
APPLICANT: Puti, Raj K.
TITLE OF INVENTION: Circularly Permuted Ligands and
TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STARTE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 174;
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colony-stimulating factor (G-CSF)"
                                                                                                                                                                                                                                                                                                                                                                      ZUNTRY: USA
ZUNTRY: USA
ZUNTRY: USA
ZUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,258
FILING DATE: 08-JAN-1997
CLASSIFICATION NUMBER: WO PCT/US95/04468
FILING DATE: 06-APR-1995
PRIOR APPLICATION NUMBER: WO PCT/US95/04468
FILING DATE: 06-APR-1995
ATTORNEY AGENT INPORMATION:
NAME: Weber, Blen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-193100US
TELEPHONE: (415) 576-0300
INPORMATION FOR JONO: 5:
SEGUIENCE CHRARACTERISTICS:
LENGTH: 174 amino acids
TWATOR ACID
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100.0%; Score 896; DB 3;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0;
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; Sequence 1, Application US/09221181
; Patent No. 6245740
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MOLECULE TYPE: protein
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OTHER INFORMATION:

OTHER INFORMATION:
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RESULT 3 US-08-722-258-5

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GENERAL INFORMATION:
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Luo, Peizh,
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: ACTIVITY
TITLE REPRENCE: A-674-2/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US 60/115,131
PRIOR FILING DATE: 1999-01-06
PRIOR FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: US 60/118,831
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.2
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1 TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                   1 TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
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GENERAL INFORMATION:
APPLICANT: COX III, George N
APPLICANT: Bolder Biotechnology, Inc.
TITLE DP INVENTION: Derivatives of Growth Hormone and Related Proteins;
FILE REPERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/09/462,941
CURRENT FILING DATE: 2000-01-14
PRIOR FILING DATE: 1997-07-14
NUMBER: OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SEC ID NO 6.
                                                                                                                                                                                                                                             121 MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
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Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0; Indels (
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; Patent No. 6627186
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ORGANISM: Homo sapiens
US-09-462-941-6
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ORGANISM: Homo sapiens
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US-09-462-941-6
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                      APPLICANT: GOLDENBERG, MERRILL
APPLICANT: SHAN, DAXIAN
APPLICANT: SHEKMAN, ALICE
TITLE OF INVENTION: POLYCL/OIL
TITLE OF INVENTION: POLYCL/OIL
TITLE OF INVENTION: POLYCL/OIL
TITLE OF INVENTION: POLYCL/OIL
TITLE OF INVENTION: PROTEINS
FILE REPRENCE: A-576
CURRENT APPLICATION NUMBER: US/09/221,181
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PARENTIN Ver. 2.0
SEQ ID NO!: 174
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Similarity 100.0%; Pred. No. 4.3e-92;
74; Conservative 0; Mismatches 0;
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100.0%; Score 896; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0;
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US-09-221-181-1
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Sequence 1, Application US/09904196B
Patent No. 655560
GENERAL INFORMATION:
APPLICANT: NISSEN, TORBEN LAUESGAARD
APPLICANT: HANSEN, CHRISTIAN TARSTEN
APPLICANT: HANSEN, CHRISTIAN TARSTEN
APPLICANT: HANSEN, CHRISTIAN MALER
ITILE OF INVENTION: G-CSF CONJUGATES
TILLE REPERENCE: 31-000700US
CURRENT PILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/760,008
PRIOR PILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/176,376
PRIOR FILING DATE: 2000-01-14
PRIOR PELLING DATE: 2000-01-15
PRIOR FILING DATE: 2000-01-15
PRIOR PELLING DATE: 2000-01-15
PRIOR APPLICATION NUMBER: 60/189,506
PRIOR PILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: DK PA 2000 00024
PRIOR PILING DATE: 2000-01-0
PRIOR PELLING DATE: 2000-01-0
PRIOR PELLING DATE: 2000-01-0
PRIOR PELLING DATE: 2000-01-0
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PRIOR PELLING DATE: 2000-01-0
PRIOR FILING DATE: 2000-01-0
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PRIOR FILING DATE: 2000-01-0
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Best Local Similarity 100.1
Matches 174; Conservative
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ORGANISM: Homo sapiens
US-09-904-1968-1
      GENERAL INFORMATION:
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                                           Length 174;
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                                      Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 174; Conservative 0; Mismatches 0;
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APPLICANT: NOSEN, TORBEN LAUESGAARD
APPLICANT: HANDEREN, KIM VILBOUR
APPLICANT: HANDEREN, KIM VILBOUR
APPLICANT: HANSEN, CHRIGTIAN KARSTEN
APPLICANT: HANSEN, CHRIGTIAN KARSTEN
TITLE REFERENCE: 31-000700US
CURRENT APPLICATION NUMBER: US/09/760,008A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/196,376
PRIOR FILING DATE: 2000-01-14/5
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-01-10
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 15
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PCT-US95-04468-5
Sequence 5, Application PC/TUS9504468
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 174; Conservative
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ORGANISM: Homo sapiens
US-09-760-008A-1
US-09-479-313B-2
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61 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120
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100.0%; Score 896; DB 5; Length 174;

Best Local Similarity 100.0%; Pred. No. 4.3e-92;

Matches 174; Conservative 0; Mismatches 0; Indels ...
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CIRCULARLY PERMUTATED LIGANDS AND CIRCULARLY PERMUTED FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL POLYPEPTIDES ENTITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL POLYPEPTIDES DERIVITIVES OF HUMAN GRANULOCYTE COLONY STIMULATING FACTOR CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/318,527
FILING DATE: 3-MAR-1989
                                                                                                                        COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04468
FILING DATE: 07-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 896; DB 6;
Pred. No. 4.3e-92;
                                                                                                                                                                                                                                                    FILING DATE: 07-APR-1955
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
ATTOMNEY/ABORI INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REPERRNEG/DOCKET NUMBER: 15280-193-1PC
TELECHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..174
OTHER INFORMATION: /label= G-CSF
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APPLICATION NUMBER: 136,647
FILING DATE: 22-DEC-1987
  TITLE OF INVENTION: CIRCULA
TITLE OF INVENTION: CIRCULA
NUMBER OF SEQUENCES: 9
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 543-960
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 174 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
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Best Local Similarity
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5194592-26
;Patent No. 5194592
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; LENGTH: 174
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                                                                            1 TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                          1 TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08010099
Patent No. 581476
GENERAL INFORMATION:
APPLICANT: OSSIUNG, Timothy
TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: Amgen Center, 1840 DeHavilland Drive
CITY: Thousand Oaks
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
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100.0%; Score 896; DB 1;
Best Local Similarity 100.0%; Pred. No. 4.4e-92;
Matches 174; Conservative 0; Mismatches 0;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: PESSIN, KAROL

REGISTRATION NUMBER: 34,899

TELECOMMUNICATION INFORMATION:

TELEPHONE: 805/499-5725

TELEPHONE: 805/499-5725

TELEPHONE: 905/499-5725
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ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
174; Conservative
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US-08-010-099-2
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Matches
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RESULT 12 US-08-167-721-1 ; Sequence 1, Application US/08167721

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61 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120
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## Patent No. 5597562
| GENERAL INFORMATION:
| APPLICANT: No. 5597562ura, Hideaki
| APPLICANT: Maruyama, Kazutoshi
| TITLE O' INVENTION: Oral Dosage Form of Biologically Active
| TITLE O'P INVENTION: Proteins
| TITLE O'P SEQUENCES: 1
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Bicknell
| ADDRESSEE: Dicknell
| ADDRESSEE: - rivet National Plaza, 20 South Clark
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                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPER PLOPPY disk
COMPUTER: PloPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,721
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/994,076
                                                                                                                                                                                                                                              ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 896; DB 1;
100.0%; Pred. No. 4.4e-92;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 11009/30403
TELECHMONICK-ION INFORMATION:
TELECHMONE: (312) 346-5750
TELEFAX: (312) 984-5740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: APPLICATION NUMBER: US/07/709,622 FILING DATE:
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US-08-428-732-6
5. Sequence 6, Application US/08428732
7. Patent No. 5606024
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APPLICANT: Boone, Thomas C.
APPLICANT: Miller, Allan L.
TITLE OF INVENTION: DNA Encod
TITLE OF INVENTION: Stimulati
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 174; Conservative
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61 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08321510
Patent No. 5824784
GENERAL INFORMATION:
APPLICANT: Kinstler, Olaf B.
APPLICANT: Gabriel, Nancy E.
APPLICANT: Farrar, Christine E.
APPLICANT: DePrince, Nandolph B.
TITLE OF INVENTION: N-Terminally Chemically Modified Protein TITLE OF INVENTION: Composition and Methods
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                   Length 175;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,510
                                                                                                                                                                                                                                                                                                            100.0%; Score 896; DB 1;
Similarity 100.0%; Pred. No. 4.4e-92;
74; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 896; DB 2; Similarity 100.0%; Pred. No. 4.4e-92; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Pessin, Karol M.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                       TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acids
805/499-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 amino acids
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                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424
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CLASSIFICATION:
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TELEPHONE:
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US-08-448-716-2
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US-08-321-510-2
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Sequence 2, Application US/08448716;
Sequence 2, Application US/08448716;
Sequence 2, Application US/08448716;
SETEMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCE: 110
CORRESPONDENCE ADDRESS: 10
CORRESPONDENCE ADDRESS: 10
CORRESPONDENCE ADDRESS: 10
CORRESPONDENCE ADGRESS: 10
CORRESPONDENCE ADGRESS: 10
CORRESPONDENCE ADGRESS: 10
CORPUTER: California
COUNTRY: United States of America
SIP: 91120-1789
COMPUTER: ISP PC Compatible
COMPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTEN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,716
FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-92;
Matches 174; Conservative 0; Mismatches 0;
                              ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 24-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
ATTOREY/AGRAT INFORMATION:
NAME: Crandall, Craig A.
REPERENCE/DOCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , TOPOLOGY: linear
, MOLECULE TYPE: protein
US-08-428-732-6
   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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61 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWQQ 120
2 TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP 61
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=	'ADFAT
	62 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALBGISPELGPTLDTLQLDVADFATTIWQQ 121
Ξ	GPTLD'
=	ISPEL
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= =	LYQGL
<u>=</u>	HSGLF
	SCLSQI
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=	SCPSO
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	DP DP

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¹²¹ MEBLGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174 qq

Search completed: October 6, 2004, 16:07:55 Job time: 34 secs

us-10-009-792c-19.rapb

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RESULT 1
                                                                                                                                                                         October 6, 2004, 16:06:41; Search time 126 Seconds (without alignments) 444.389 Million cell updates/sec
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896
1 TPLGPASSLPQSFLLKCLEQ.....SHLQSFLEVSYRVLRHLAQP 174
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1. /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2. /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
3. /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1351062 segs, 321799191 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score: 8
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 1, Appli	Sequence 2, Appli		Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	H	Sequence 1, Appli	H	9	Ļ	9	ý
		ΠD	US-09-760-008A-1	US-09-950-473-2	US-09-921-114-1	US-09-950-123-2	US-10-411-037-2	US-10-411-026-2	US-10-467-396-1	US-10-436-784-1	US-10-016-403-1	US-10-003-496-1	US-10-192-294-1	US-10-009-792A-19	US-10-318-966-1	US-10-400-377-6	US-10-400-708-6
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		Match Length DB	174	174	174	174	174	174	174	174	174	174	174	174	174	174	174
₩	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score	968	968	968	968	896	896	968	968	968	968	968	896	896	968	896
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Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 37, Appli Sequence 1, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 15, Appli	
14 US-10-298-148-6 16 US-10-410-962-2 16 US-10-612-695-2 16 US-10-612-695-2 16 US-10-612-695-2 16 US-10-410-997-2 16 US-10-410-997-2 16 US-10-410-997-2 16 US-10-750-994-2 16 US-10-750-994-2 16 US-10-750-994-2 16 US-10-750-994-2 17 US-10-750-995-3 18 US-10-730-996-3 19 US-09-230-733-1 2 US-09-230-733-1 3 US-10-895-2 14 US-10-925-3-1 14 US-10-925-3-1 15 US-10-925-3-1 16 US-10-925-3-1 17 US-10-925-3-1 18 US-10-925-3-1 19 US-10-659-295-38 16 US-10-659-295-38 16 US-10-659-295-3	
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ALIGNMENTS

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08A		NISSEN, TORBEN LAUESGAARD	pg.	HANSEN, CHRISTIAN KARSTEN	œ	ATES	FILE REFERENCE: 31-000700US	09//6	T FILING DATE: 2001-05-11	0/0/	APPLICATION NUMBER: 60/189,506		,644		APPLICATION NUMBER: DK PA 2000 (2000 (2000									Score 896; DB 9;	Misn
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ı poli	ZOOZ	ISSE	ANDERSEN, KIM VILBOUR	HANS	MIKKELSEN, JAN MOLLER	ENTI	Ξ	ICAT	CURRENT FILING DATE: 2001-05-11	AFFILIAN NOMBER: 80/ FILIAN DATE: 2000-01-14	ATIO	FILING DATE:	APPLICATION NUMBER: 60/215,644	FILING DATE:	ATIO	DATE:	APPLICATION NUMBER: DK PA	FILING DATE:	APPLICATION NUMBER: DK PA	DAT	SEQ ID NOS: 15	PatentIn Ver.				ORGANISM: Homo sapiens	_	η 	0
08A- 1, A	NFOR	Z ::			 H	NI	EREN	APPL	FILL) (Z.T.)	PLIC	LING	PLIC	LING	PLIC	FILING	PLIC	LING	PLIC	LING		. Pa	н	174	RΤ	M .: M	08A-	ch riv	174;
60-0 nce	AI NO	ICAN	ICAN	ICAN	ICAN	8 0	REF	EN I	ENE				-		-				RAP	E E	ER OF	WARE	8	LENGTH: 174	TYPE: PRT	ANIS	0-09	Mat	5 0 0 0 0
US-09-760-008A-1 ; Sequence 1, Ap	Patent No. US20020004483A1 GENERAL INFORMATION:	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	TITLE OF INVENTION: G-CSF CONJUGATES	FILE	CURR	CURRE	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR FILING DATE: 2000-06-16	NUMBER	SOFTWARE:	SEQ ID NO 1	LEK	TYP	ORG	US-09-760-008A-1	Query Match Best Local Similarity	Matches
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Tue Oct 12 09:18:48 2004

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DB 9; Length 174;
 100.0%; Score 896;
    Query Match
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GENERAL INFOGRATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: GALACTOSIDASE A
FILE REPRENCE: 040853-01-5082
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FLLING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120
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100.0%; Score 896; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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                                                                                     61 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALBGISPELGPTLDTLQLDVADFATTIWQQ 120
                                                         61 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120
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1 TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP 60
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                                                                                                                                                         121 MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 174;
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                                                                                                                                                                                                                                                                                                        GENERAL INPORMATION:
APPLICANT: Sarkar, Casim
APPLICANT: Sarkar, Casim
APPLICANT: Lauffenburger, Douglas
TITLE OF INVENTION: G-CSF Analog Compositions and Methods
FILE REFERENCE: 01017/37732
CURRENT APPLICATION NUMBER: US/09/950,473
CURRENT PILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 896; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 174
TYPE: PRT
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US-09-950-473-2
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Sequence 2, Application US/09950123
Publication No. US2030166527A1
Publication No. US2030166527A1
Publication No. US2030166527A1
APPLICANT: Sarkar, Casim
APPLICANT: Lauffenburger, Douglas
APPLICANT: Tack, Bruce
TITLE REPERENCE: 01017/373777
FILLE REPERENCE: 01017/373777
CURRENT APPLICATION NUMBER: US/09/950,123
CURRENT APPLICATION NUMBER: 2001-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
                             Indels
Pred. No. 2.3e-85; Mismatches 0;
  Best Local Similarity 100.0%; P
Matches 174; Conservative 0;
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                                      Query Match 100.0%; Score 896; DB 12; Length 174; Best Local Similarity 100.0%; Pred. No. 2.3e-85; Matches 174; Conservative 0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0;
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Publication No. US20030204057A1
GENERAL INFORMATION:
APPLICANT: ISHIKAWA ET AL
ITLE OF INVENTION: CHEMICALLY-MODIFIED G-CSF
FILE REFERENCE: 11009/561934.
CURRENT APPLICATION NUMBER: US/10/436,784
CURRENT FILING DATE: 2003-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo Sapien
US-10-467-396-1
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US-10-411-026

Publication No. US20040063911A1

GENERAL INFORMATION:

APPLICANT: DeFrees, Shawn
APPLICANT: Bayer Robert
APPLICANT: Bayer Robert
APPLICANT: Bayer Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: APPLICANT: Bayer ROBELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: PROTEIN REWODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHODS
FILE REFERENCE: 0003-04-09
FILE REPRENCE: 2003-04-09
FRICK PILING DATE: 2003-04-09
FRICK FILING DATE: 2003-04-09
FRICK FILING DATE: 2003-04-09
FRICK APPLICATION NUMBER: US 60/384,692
FRICK FILING DATE: 2003-06-07
FRICK FILING DATE: 2003-06-08
FRICK FILING DATE: 2003-06-08
FRICK FILING DATE: 2003-08-08
FRICK FILING DATE: 2003-08
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PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-27
PRIOR FILING DATE: 2002-06-25
PRIOR PLING DATE: 2002-06-25
PRIOR PELICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR PLING DATE: 2002-07-17
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR PRIOR OF SEQ ID NOS: 75
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-411-037-2
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; ORGANISM: Homo sapiens
US-10-411-026-2
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TYPE: PRT
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61 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120
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Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                              Length 174;
                                                                                                                                                                                                             Indels
. LOCATION: 1..174

; OTHER INFORMATION: /note= "granulocyte-colony

stimulating factor"

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-016-403-1
                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1. Application US/10003496
; Sequence 1. Application US/10003496
; Publication No. US2020142964A1
; GENERAL INFORMATION:
    APPLICANT: Maxygen ApS
; APPLICANT: Maxygen Holdings Ltd.
    TITLE OF INVENTION: Single-Chain Polypeptides
; TITLE REFERENCE: 021648210
; CURRENT FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2002-01-31
; PRIOR PLLICATION NUMBER: US 60/245,727
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
; TEND NO. 1
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US-10-199-294-1
Sequence 1, Application US/10192294
Publication No. US20030118612A1
GENERAL INFORMATION:
APPLICANT: NISSEN, Torben Lauesgaard
TITLE OF INVENTION: G-CSF Conjugates
FILE REFERENCE: 02508310
CURRENT APPLICATION NUMBER: US/10/192,294
CURRENT FILING DATE: 2002-07-10
PRIOR PELICATION NUMBER: US 09/904,196
PRIOR FILING DATE: 2001-07-11
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ORGANISM: Homo sapiens
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ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
STREET: 25 West Main Street
                                                                                                                                                                                                                                                                                                                                                               Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/10/016,403
FILING DATE: 10-Dec-2001
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10016403
Publication No. US20020107505A1
GENERAL INFORMATION:
APPLICANT: Holladay, Leslie A.
APPLICANT: Holladay, Leslie A.
ITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS
TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 896; DB 12; Best Local Similarity 100.0%; Pred. No. 2.3e-85; Matches 174; Conservative 0; Mismatches 0;
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REGISTRATION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 8734.28
TELECOMMUNICATION INFORMATION:
                        PRIOR APPLICATION NUMBER: US 09/518,896
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 08/957,719
PRIOR FILING DATE: 1997-10-27
PRIOR PELING DATE: 1992-11-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 174
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APPLICATION NUMBER: 08/466,610

FILING DATE: 1995-JUN-06

ATTORNEY/AGENT INFORMATION:
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TELEFAX: 608-257-7643
NN FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Madison STATE: WI
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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US20030158375A1

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US-10-318-966-1
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; Sequence 19, Application US/10009792A
; Publication No. US20030153049A1
; GENERAL INFORMATION:
    APPLICANT: LEE, Sang-Yup
; APPLICANT: LEE, Sang-Yup
; APPLICANT: LEE, SecHERICHIA COLI STRAIN SECRETING HUMAN
; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
; TITLE OF INVENTION: ERANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
; FILE REFERENCE: HYLEEGO, ODAPC
; CURRENT APPLICATION NUMBER: US/10/009, 792A
; CURRENT FILING DATE: 2001-03-31
; PRIOR APPLICANTION NUMBER: KR 10-2000-0017052
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 174
; TYPE: PRI

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100.0%; Score 896; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: DK PA 2002 00447
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: DK PA 2002 00708
PRIOR FILING DATE: 2002-05-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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US-10-318-966-1
; Sequence 1, Application US/10318966
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Matches 174; Conservative
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US-10-009-792A-19
                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Publication No. US20030166865A1

GENERAL INFORMATION

APPLICANT: Cox III, George N

APPLICANT: Bolder Biotechnology, Inc.

TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

TITLE OF INVENTION NUMBER: US/10/400, 708

CURRENT APPLICATION NUMBER: US/09/462,941

PRIOR APPLICATION NUMBER: US/09/462,941

PRIOR APPLICATION NUMBER: 60/052,516

PRIOR APPLICATION NUMBER: 60/052,516

PRIOR PLING DATE: 1997-07-14

PRIOR PLING DATE: 1997-07-14

PRIOR FILING DATE: 1997-07-14

PRIOR FILING DATE: 1997-07-14

PRIOR FILING DATE: 1997-07-14

TYPE: PRIOR PLING PAID: PRIORS: 41

COSTUMARE: PatentIN Ver. 2.0

SEQ ID NO 6

LENGTH: 174

TYPE: PRI

TYPE: TYPE: PRI

TYPE: TY
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Matches 174; Conservative 0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Pred. No. 2.3e-85;
Matches 174; Conservative 0; Mismatches 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 6, 2004, 15:59:42; Search time 39 Seconds (without alignments) 429.162 Million cell updates/sec Run on:

US-10-009-792C-19 896 1 TPLGPASSLPQSFLLKCLEQ.....SHLQSFLEVSYRVLRHLAQP Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

scr	granulocyte	d)		(1)	granulocyte colony	granulocyte colony	myelomonocytic gro	디	interleukin 6 - pi	interleukin-6 prec	hypothetical prote	homeotic protein c	oligopeptide trans	probable sensor/re	interleukin-6 prec	H+-transporting tw	interleukin 6 - ca	conserved hypothet	aryl hydrocarbon r	probable threonyl-	probable D-alanyl-	hypothetical prote	pro	yrate		homoserine kinase		two-component hybr	ciliary neurotroph
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 FOHUGL FOHUGL FOHUGL STANDIOCYTE colony-stimulating factor precursor - human N;Alternate names: colony-stimulating factor 3; G-CSF C;Species: Homo sapiens (man)
	C;Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change_22-Jun-1999 C;Accession: A25093; A49796; A47587; S68331 R;Nagata, S; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Hirata, Y.; Kubota, N.; Oheda, M.; EMBO J. S, 575-581, 1986
	A; Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-stim A; Reference number: A25093; MUID:86220137; PMID:2423327 A; Accession: A25093; MUID:86220137; PMID:2423327 A; Accession: A25093 A; mRNA
	A, Residues: 1-204 <nag> A, Cross-references: EMBL:X03656; EMBL:X03655; NID:g31693; PIDN:CAA27290.1; PID:g732764 R, Devlin, J.J.; Devlin, P.E.; Myambo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.</nag>
	J. Leukoc. Blol. 41, 302-306, 1398 / A. Title: Expression of granulocyte colony-stimulating factor by human cell lines. A; Title: Expression of granulocyte colony-stimulating factor by human cell lines. A; Reference number: A49796; MUID:87196936; PMID:3494801
	AjMolecule Lype: mana AjResdues: 1-204 «DBV» AjCross-references: GB:M17706; NID:g183040; PIDN:AAA35882.1; PID:g183041 RjSouza, L.M.; Boone, T.C.; Gabrilove, J.; Lai, P.H.; Zsebo, K.M.; Murdock, D.C.; Chazi:
	Science 232, 61-65, 1986 A; Title: Recombinant human granulocyte colony-stimulating factor: effects on normal and A; Reference number: A47587; MUID:86151684; PMID:2420009 A; Accession: A47587
	A; Molecule type: mRNA A; Residues: 19-204 <scu> A; Residues: 19-204 <scu> A; Cross-references: GB:M13008; NID:g183044; PIDN:AAA03056.1; PID:g183045 A; Cross-references: GB:M13008; NID:g183044; PIDN:AAA03056.1; PID:g183045 B; Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F. Arch Riochem, Riochem, Riochem, Riochem, Riochem, Riochem</scu></scu>
	A;Title: Extracellular domain of granulocyte-colony stimulating factor receptor. A;Reference number: S68331; MUID:96132662; PMID:8554326 A;Accession: S68331
	A;Molecule type: protein A;Molecule type: HAN> C;Genetics:
-	A,Gene: GDB:CSF3 A;Cross-references: GDB:119083; OMIM:138970 A;Map position: 17q11.2-17q12 A;Introns: 14/1; 65/3; 101/3; 150/3
	C,Function: A,Poscaription: stimulates the differentiation and proliferation of hematopoietic progen. A,Poscaription: stimulates the differentiation and proliferation of hematopoietic progen. C,Superfamily: interleukin-6 C,Keywords: cytckine; glycoprotein; growth factor; macrophage; monomer F;1-30,Omain: signal sequence #status predicted <sig>F;31-204/Product: granulocyte colony-stimulating factor #status predicted <mat>F;66-72,94-104/Disulfide bonds: #status predicted</mat></sig>

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Gaps

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Indels

Length 194;

120 140

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A;Residues: 1-194 A;Cross-references: EMBL:Y08558
A;Cross-references: EMBL:Y08558
C;Function:
A;Description: stimulates the differentiation and proliferation ofhematopoietic progenit
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor; macrophage
C;Keywords: cytokine; growth factor; macrophage
F;1-20/Domain: signal sequence (fragment) #status predicted <SIG>F;21-194/Product: granulocyte colony-stimulating factor #status predicted <MAT>
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A; Residues: 1-174 < OBR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. Accession: A24573
A. Cross-references: ENBL:X03438; NID:g31689; PIDN:CAA27168.1; PID:g31690
C. Comment: This variant splice form is not expressed in three other cell lines and may z C. Genetics:
A. Genetics:
A. Genetics:
A. Access references: GDB:119083; OMIM:138970
A. Map position: 1791.2-179.2
A. And position: 1791.2-179.3
A. Introns: 14/1; 68/3; 104/3; 153/3
C. Superfamily: interleukin-6
C. Keywords: cytckine; glycoprotein; growth factor; macrophage; monomer
F. H. 30/Opmain: signal sequence Hestatus predicted < SIG>
F. S1-207/Product: granulocyte colony-stimulating factor variant splice form CHU-2 #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                granulocyte colony-stimulating factor precursor variant splice form CHU-2 - human N;Alternate names: colony-stimulating factor 3; G-CSF C;Species: Homo sapiens (man) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999 C;Accession: A24573 Fs.Nagata, S.; Tsuchiya, M.; Asano, S.; Kaziro, Y.; Yamazaki, T.; Yamamoto, O.; Hirata, Nature 319, 415-418, 1986 A;Aritle: Molecular cloning and expression of cDNA for human granulocyte colony-stimulatine. A;Reference number: A24573; MUID:86118679; PMID:3484805
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                                                                                                                                                                                                           LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120
                                                                                                                                                                                                                                                           LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 WQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WQQMEELGWAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulocyte colony-stimulating factor precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Jun-2000
                                                                                                                                                      TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                                                                       1 TPLGPASSIPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
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  Length 204;
                                                     Indels
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Query Match
100.0%; Score 896; DB 1;
Best Local Similarity 100.0%; Pred. No. 7.8e-78;
Matches 174; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.7%; Score 884.5; DB 2
98.3%; Pred. No. 9.9e-77;
iive 0; Mismatches 0
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Best Local Similarity 98.3
Matches 174; Conservative
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granulocyte colony-stimulating factor - sheep (fragment)
(;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
(;Dacession: T10268
R;O'Brien, P.M.; Seow, H.F.; Rothel, J.S.; Wood, P.R.
A;Title: Cloning and sequencing of an ovine granulocyte colony-stimulating factor cDNA.
A;Reference number: Z17009; MUID:95102116; PMID:7528579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hematopoletic progen:
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C.Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change 16-Jul-1999
C.Accession: A29536; A26496; $02493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPLGPARSLPQSFLLKCLEQVRKIQADGASLQERLCATHKLCHPESLVLLGHSLGIPQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 .LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
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                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: L07939; NID: 9310381; PIDN: AAA68006.1; PID: 9310382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
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82.2%; Pred. No. 6.9e-63;
.ive 10; Mismatches 21.
                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Superfamily: interleukin-6
C,Keywords: cytokine; growth factor; macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granulocyte colony-stimulating factor N;Alternate names: G-CSF
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C,Superfamily: interleukin-6
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September 1996 l expression of feline granulocyte colony stimulating

A;Status: preliminary; translated from GB/EMBL/DDBJ

C,Accession: T09255 R;Dunham, S.P.; Onions, D.E. submitted to the EMBL Data Library, S. A;Description: Cloning, sequence and A;Reference number: Z16630 A;Reference number: Z16630

149

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Rileutz, A.; Damm, K.; Sterneck, E.; Kowenz, E.; Ness, S.; Frank, R.; Gausepohl, H.; Parkiettz, A.; Damm, K.; Sterneck, E.; Kowenz, E.; Ness, S.; Frank, R.; Gausepohl, H.; Parkieteller Molecular cloning of the chicken myelomonocytic growth factor (cMGF) reveals r. A; Reference number: 803633, MUID:89231616; PMID:2785450
A; Reference number: 803633, MUID:89231616; PMID:2785450
A; Residence number: BNBA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residuate: 1-201 cLEU-
A; Cross-references: EMBL:X14477; NID:g63596; PIDN:CAA32639.1; PID:g63597
C; Superfamily: interleukin-6
C; Superfamily: interleukin-6
C; Keywords: glycoprotein-
F; 1-23/Domain: signal sequence #status predicted cAGF
F; 1-23/Domain: signal sequencytic growth factor #status predicted cAGT>
F; 24-201/Product: myelomonocytic growth factor #status predicted
F; 123, 137/Binding site: carbohydrate (Asn) (covalent) #status predicted
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prointerleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C;Accession: 146621
R;Richards, C:; Saklatva, J.
Cytokine 3, 269-276, 1991
A;Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of A;Reference number: 146621, MUID: 91338547; PMID: 1873476
A;Accession: 146621
A;Accession: 146621
A;Accession: Ide621
A;Accession: Ide621
A;Residuary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residuars: 1-212 <RIC>
A;Gross-references: GB:M86722; NID: 9164624; PIDN: AAC37333.1; PID: 9164625
C;Genetics:
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rank, R.; Gausepohl, H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                       myelomonocytic growth factor precursor - chicken
NyAlternate names: colony-stimulating factor cMGF
C;Species: Gallus gallus (chicken)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A42247, 803633
R;Sterneck, E.; Blattner, C.; Graf, T.; Leutz, A.
Mol. Cell. Biol. 12, 1728-1735, 1992
A;Title: Structure of the chicken myelomonocytic growth factor gene and spec A;Reference number: A42247; MUID:92195319; PMID:1549124
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                                                                          90 SCSSQALQQTXCLSQLHSGLFLYQGLLQALAGISSBLAPTLDMLHLDVDNFATTIWQQMB
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Best Local
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C.Species: Ratus norvegicus (Norway rat)
C.Species: Ratus norvegicus (Norway rat)
C.Species: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 16-Jul-1999
C.Accession: UCS043
R.Han, S.W.; Ramesh, N.; Osborne, W.R.A.
G.Accession: UCS043
A.Reference number: UCS043; MUID:97074656; PMID:8917083
A.Accession: UCS043
A.Residues: 1-214 cHAN.A
A.Residues: 1-214 cHAN.A
A.Residues: 1-214 cHAN.A
A.Residues: 1-214 cHAN.A
A.Residues: Comment: This receptor acts on precursor hemapoietic cells to control the production a C:Comment: This receptor acts on precursor hemapoietic cells to control the production a C:Comment: This receptor acts on precursor hemapoietic cells to control the production a C:Comment: This receptor acts on precursor hemapoietic cells to control the production a C:Comment: Signal sequence #status predicted <SIG>F:1-21/Domain: signal sequence #status predicted <SIG>F:2-214/Product: granulocyte colony-stimulating factor #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                    murine granulocyte colony-stimul
                                                                          factor
                                                                      r murine granulocyte colony-stimulating PMID:3494605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGPASSLPQSFILKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 LPPSLPLPRSFLLKSLEQVRKIQASGSVLLEQLCATYKLCHPEELVLLGHSLGIPKASLS
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                                                                                                                                                                                                                                                   A;Cross-references: GB:X05402; NID:g51059; PIDN:CAA28986.1; PID:g51060 R;Tsuchiya, M.; Asano, S.; Kaziro, Y.; Nagata, S. Proc. Natl. Acad. Sci. U.S.A. 83, 7633-7637, 1986 A;Title: Isolation and characterization of the cDNA for murine granuloc A;Reference number: A26496; MUID:87017003; PMID:3489940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 ELGMAPALQPIQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 208;
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Pred. No. 1.4e-53;
9; Mismatches 32;
R;Tsuchiya, M.; Kaziro, Y.; Nagata, S.
Bur. J. Biochem. 165, 7-12, 1987
A;Title: Activationsomal gene structure for
A;Reference number: A29536; MUID:87190474; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.5%;
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Matches 129; Conservative
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                                                                                                                                                                                                                       Residues: 1-208 <TSU>
                                                                                                                                                    A, Accession: A29536
A; Molecule type: DNA
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Best Local Simi
Matches 127;
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C; Keywords: cytokine; growth factor
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A;Residues: 1-2175 <BLO>
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C,Species: Sus scrofa domestica (domestic pig)
C,Species: Sus scrofa domestica (domestic pig)
C,Date: 21-Reb-1997 #sequence_revision 21-Reb-1997 #text_change 16-Jul-1999
C,Accession: 146590
R,Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A,Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conce A,Reference number: 146590
A,Accession: 146590
A,Accession: 146590
A,Retaria preliminary, translated from GB/EMBL/DDBJ
A,Rotheule type: mRNA
A,Residues: 1-212 < MAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-6 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Species: Lauru-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
C;Accession: 10-3016
R;Swiderski, C.E.; Horohov, D.W.
submitted to the EMBL Data Library, July 1996
A;Reference number: 216613
A;Accession: T09216
A;Statuus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-208 <SWIP
A;Cross-references: EMBL:U64794; NID:g2654388
C;Genetics:
A;Gene: IL-6
C;Superfamily: interleukin-6
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                                                                                                                                                             LSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGWAPALQPT- 133
                                                                                                                                                                                                                                           75 LSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPT- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                      16 KCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP-WAPLSSCPSQALQLAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 KCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP-WAPLSSCPSQALQLAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KTEELIKY ILGKI SAMRKEMČEKYEKČENSKEVLAENNINI PKMAEKDGČFQSGFNQETČ
                                                                                                Gaps
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A)Gene: IL-6
C)Superfamily: interleukin-6
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                                                        Length 212;
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                                                                                                                                                                                                                                                                                                -QGAMPAFAS--AFQRRAGGVLVASHLQSFLEVSYRVLR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 -QGAMPAFAS--AFQRRAGGVLVASHLQSFLEVSYRVLR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.72 NAGLLDKLOSONEWMKNTKIILILRSLEDFLOFSLRAIR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%; Score 106.5; DB 2; ilarity 22.6%; Pred. No. 0.01; Conservative 33; Mismatches 85;
                                                                                              85;
                                                        DB 2;
                                                      11.9%; Score 106.5; DE 22.6%; Pred. No. 0.01; iive 33; Mismatches
                                                                                              Conservative
A,Gene: IL6
C,Superfamily: interleukin-6
                                            Query Match
Best Local Similarity
Matches 36; Conserv
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Best Local Similarity
Matches 36; Conserv
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hypothetical protein VC0886 [imported] - Vibrio cholerae (strain N16961 serogroup O1) Cispecies: Vibrio cholerae (spaces: Vibrio cholerae) (spaces: Vibr
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Nature 333, 629-635, 1988
A;Title: Primary structure and expression of a product from cut, a locus involved in spe
A;Reference number: S03170; MJID:88232956; PMID:2897632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 KMAEKDGCFQSGFNQETCLMKITTGLSEFQIYLEYLQNEFKGEKENIKTMQISTKVLVQI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 -WAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S---CPSQALQLAGCLSQ-1HSGLFLYQGLLQALEGI-----SPELGPTLDTLQ 107
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C,Species: Drosophila melanogaster
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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C;Superfamily: homeotic protein cut; cut repeat homology; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                  2 PLGPASSLPQSFLL----KCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 IWQQMEELGMA---PALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |:|: | : | : | : | : | : | : | IMQKOMKNPEVTTPDDPTAKSSLLAKLHSQNEWLKNTTTHLILRSLEDFLQFSLRAVR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Gaps
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                                                                                                                               Indels
Query Match
11.2%; Score 100; DB 2; L.
Best Local Similarity 21.6%; Pred. No. 0.041;
Matches 38; Conservative 35; Mismatches 95;
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-LGPTLDTLQLDVADFATTIWQQMEELGMA 127

53;

Indels

49;

Mismatches

Length 786;

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26 GDGAALQEKLC-ATYKLCHPEELVLLG--HSLGIPWAPLSSCPSQALQLAG-CLSQLHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALQPTQGAMPAFASAFQRRAGGVLVASHLQSFL--EVSYRV--LRHLAQP 174
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                                                                                                                 Score 88.5; DB 2;
Pred. No. 2.5;
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   strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin-6 precursor - bovine
                                                                                                                                                                                                                                                                                                                                                      82 LFLYQGLLQALEGISPE-
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Best Local Similarity 20.5$
Marches 36; Conservative
                                                                                                                                                                            Conservative
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                                                                                                                    Query Match
Best Local Similarity
Matches 50; Conserv
      source:
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A;Experimental s
C;Genetics:
A;Gene: PA2824
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R, Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradan, S.J.; Warrener, P.; Hickey, M.J.; Bradan, S.J.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jacory, S.; Olson, M.W.
Nature 406, 959-964, 2000
A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A, Reference number: A82950; MUD:20437337; PMID:10984043
A, Accession: F83292
A, Accession: P83292
A, Accession: Carrier DNA
A, Residues: 1-786 < STO>
A, Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG06212.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R. Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon D.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A.Title: Complete Genome Sequence of Caulobacter crescentus.
A.Reference number: A87249; MUID:21173698; PMID:11259647
A.Status: preliminary
A.Status: preliminary
A.Residues: 1-666 < STO>
A.Cross-references: GB:AB005673; NID:g13424225; PIDN:AAK24613.1; GSPDB:GN00148
C.; Genetics:
A.Genetics:
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C,Species: Pseudomonas aeruginosa
C,Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                        GLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQR 146
                                                                                                                                                                                                                                                                       27 DGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLSQLHSGLFLYQ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: A87577
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F;886-958/Domain: cut repeat homology <CUI>F;1339-1411/Domain: cut repeat homology <CUZ>F;1617-1689/Domain: cut repeat homology <CUZ>F;146-1802/Domain: homeobox homology <HOX>
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Matches 35; Conser
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Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cispate: 10-8ep-1999 #sequence_revision 10-8ep-1999 #text_change 10-8ep-1999
Ciscession: A56610; S2162
Ribrosomans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
DNA Seq. 2., 411-413, 1992
A;Title: Nucleoride sequence of bovine interleukin-6 cDNA.
A;Reference number: A56610; MUID:93076003; PMID:1446077
A;Status: preliminary
A;Molecule rype: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLG---PASSLPQSFLLKCLEQ----VRKIQGDGAALQEKLCATYKLCHPEELVLLGHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 ATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLR 169
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8
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                                                                                                                                                                                                                                                                 A; residues: 1-208 corRo>
A; Cross-references: EMBL:X57317; NID:g2193; PIDN:CAA40572.1;
A; Experimental source: BLV induced B cell-lymphosarcoma
A; Note: sequence extracted from NCBI backbone (NCBIP:118917)
C; Superfamily: interleukin-6
C; Keywords: cytokine
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 6, 2004, 15:51:18; Search time 23 Seconds (without alignments) 393.922 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-009-792C-19 896 1 TPLGPASSLPQSFLLKCLEQ.....SHLQSFLEVSYRVLRHLAQP 174

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 Total number of hits satisfying chosen parameters:

141681 segs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

- 6	Description Description	919 homo sa	708 felis s	746 ovi	334 canis f	333 bos tau	337 sus s	Ε	4 gallu	sus scr	orcinu	ednna		Ο.	pos	phoca	capr		aeropyrum	ΰ	m geranylg	ũ	neisseria	gallus gal	b geranylg	shigella	brassica n	homod	sacch	parsi	homod	homod	P05231 homo sapien	19 homo sa
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P49327 homo sapien P23908 escherichia P95122 mycobacteri P83714 mus musculu Q05233 mycobacteri P89557 vibrio vuln Q8x742 escherichia Q8kb97 escherichia Q9k912 homo sapien Q95749 h geranylge O65726 brassica na Q99062 homo sapien
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ALIGNMENTS

RESULT 1 COF 3 HUME DD

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AF388025; AAK62469.1; -. M17706; AAA35882.1; -.
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EMBL, M13008, AAA03056.1, -.
EMBL, X03656, CAA27291.1, -.
EMBL, X03655, CAA27290.1, -.
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PDB; 1GNC; 31-JUL-94.
PDB; 1CD9; 08-MAR-00.
PDB; 1PGR; 08-MAR-00.
Genew; HGNC:2438; CSF3.
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A25093; FQHUGL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=92281718; PubMed=7685117;
MEDLINE=92281718; PubMed=7685117;
The structure of granulocyte-colony-stimulating factor and its
relationship to other growth factors.";
Proc. Natl. Acad. Sci. U.S.A. 90:5167-5711(1993).
-!-FUNCTION: GRANULOCYTE/WARROPHAGE COLONY-STIMULATING FACTORS ARE
CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
DIFFERENTATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
CSP INDUCES GRANULOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHARMACEUTICAL: Available under the names Neupogen or Granulokine (Amgen/Roche) and Granocyte (Rhone-Poulenc). Used to treat neutroppinia (a disorder characterized by an extremely low number of neutrophils in blood).

SIMILARITY: Belongs to the IL-6 superfamily.

CAUTION: REP. 4 MISQUOTES THE GENE NAME AS "CSFI".

DATABAGE: NAME=Neupogen/Granulokine;

NOTE=Clinical information on Neupogen/Granulokine;
"Glycosidase digestion, electrophoresis and chromatographic analysis of recombinant human granulocyte colony-stimulating factor glycoforms produced in Chinese hamter ovary cells."; J. Chromatogr. A 637:55-62(1993).
                                                                                                                                                                                                                                                                                                                                                        Zink T., Ross A., Iners K., Cleslar C., Rudolph R., Holak T.A.; "Structure and dynamics of the human granulocyte colony-stimulating factor determined by NMR spectroscopy. Loop mobility in a four-helix-bundle protein.";
                                                                                                                                 STRUCTURE BY NMR.
MEDLINE=93106200; PubMed=1281794;
Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
"Secondary structure of human granulocyte colony-stimulating factor derived from NMR spectroscopy.";
FEBS Lett. 314:435-439(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Short;
IsoId=P09919-2; Sequence=VSP 002673;
PTM: O-GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH CAN BE
MODIFIED WITH UP TO TWO SIALIC ACID RESIDUES (DONE IN
RECOMBINANTLY EXPRESSED G-CSF FROM CHO CELLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
Name-Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P09919-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR.
MEDLINE=94304859; PubMed=7518249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 WAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005130; F:granulocyte colony-stimulating factor recep. . .; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003629; GCSF MGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 WQQMBELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKL---CATYKLCHPEELVLLGHSLGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 WAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                            SMART; SM00126; IL6; 1. PROSITE; SM00126; IL6; 1. PROSITE; PS00254; ILFRLEUKIN 6; 1. Cytokine; Ps00254; INTERLEUKIN 6; 1. Cytokine; Growth factor; Glycoprotein; Signal; Alternative splicing; Polymorphism; Pharmaceutical; 3D-structure. 1. 30
                                                                                                                                                                                                                                                        O-LINKED (GALNAC. . .) (BY SIMILARITY).
Missing (in isoform Short).
/FIId=VSP_002673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment)
                                                                                                                                                                                                                GRANULOCYTE COLONY-STIMULATING FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202
22293 MW; 421F635ECC776996 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.7%; Score 884.5; DB 1;
98.3%; Pred. No. 3.1e-74;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                          A -> T.
/FTId=VAR_013074.
                                                                                                                                                                                                                                                                                                                           FTIG=VAR_013073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Buropean shorthair; TISSUE=Lung;
MEDLINS389237; PubMed=11497496;
Dunham S.P., Onions D.E.;
                                                                                       Pfam; PR00489; IL6; 1.
PRINTS; PR00433; IL6GCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 98.3
Matches 174; Conservative
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                                                                                                                                                                                                      30
207
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107
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86
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1124
1127
1132
203
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                                                                                                                                                                                                                                                                                                                                          174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 ;
207 AA;
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                                                                                                                                                                                                                    31
69
97
166
66
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69
77
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87
1125
1130
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002708;
                                                                                                                                                                                                                                  DISULFID
DISULFID
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                            VARIANT
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CSF 2 FELCA
CSF 2 FELCA
CSF 3 C 00.270
DT 30.MAY.
DT 10.OCT.
DE Granul
GN Felis
CSF Felis
CN MANAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120
                                                                                                                                                       DNA Seq. 4:339-342 (1994).

-!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESIES BY CONTROLLING THE RODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS CSF INDUCES GRANULOCYTES (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            much entities ic.,
or send an email to.
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C.
DR PIEL; L07939; AAA68006.1; ..
DR HSSP; p3833; 18GC.
DR HSSP; p3833; 18GC.
DR HSSP; p803359; GCSF MGF.
DR Proposition of the propositi
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Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIM: O-glycosylated (By similarity). SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Granulocyte colony-stimulating factor (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 AA
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                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomer.
SUBCBLLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 82.2<sup>3</sup>
Matches 143; Conservative
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                                                                                                                                   factor cDNA.";
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01-JUN-1994 (
28-FEB-2003 (
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ID CSF3_CANFA

ID CSF3_CANFA

DT 01-JUN-

DT 28-FEB-

DE Granulo

GN CSF3.

CS Canis

COC Mammali

OC MAmmali

OC MAMMINI

IN II

RP X-RAY C

RP X-RAY C

RR MC MELINE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Isolation, nucleotide sequence and expression of a cDNA encoding feline granulocyte colony-stimulating factor."; Cytokine 14:347-351 (2001).

-!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS CSF INDUCES GRANULOCYTES (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Screted.
-!- FUM: O-glycosylated (By similarity).
-!- SIMILARITY: Belongs to the IL-6 superfamily.
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F72B7AB3DAE7385E CRC64;
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BY SIMILARITY.
BY SIMILARITY.
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COF13 vits arises (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y08558; CAA69853.1; -.
PIR; T09255, T09255.
HSSP; PS884; IBGE.
InterPro; IPR003629; GCSF MGF.
InterPro; IPR003629; IL6 MGF GCSF.
Pfam; PF00489; IL6; 1.
PRINTS; PR0043; IL6GCSFMGF.
Propon; PD008389; GCSF MGF; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
Cytokine; Growth factor; Glycoprotein; Signal.
NON TRR <1 20 POTENTIAL.
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30-MAY-2000 (Rel. 39, Last sequence update)
36-FEB-2003 (Rel. 41, Last annotation update)
Granulocyte colony-stimulating factor (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
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76 62
76 94
153
153 0 P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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CSF3 SHEEP
ID CSF3 SHEEP
AC Q28746;
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Matches 141;
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120

X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS). MEDLINE=94076341; PubMed=7504736; Lovejoy B., Cascio D., Eisenberg D.;

SEQUENCE FROM N.A.

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Sest Local Simi
Watches 141;
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SEQUENCE
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AC P35833, 097V89;
DT 01-UDN-1994 (Rel. 29, Created)
DT 01-UDN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 41, Last annotation update)
DT 28-FBB-2003 (Rel. 41, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN BOS taurus (Bovine).
OC BOY GESP.
OC BOY GROWINE).
DC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
NN NCBI_TaxID=9913;
N [1]
"Crystal structure of canine and bovine granulocyte-colony stimulating factor (G-CSF).";

9. Mol. Biol. 234:640-653(1993).

1. FUNCTION: GRANULOCYTE/WACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESTS BY CONTROLLING THE PRODUCTION, DIFFERRMITATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS CSF INDUCES GRANULOCYTES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Indels
                                                                                                                                                                                                                                            InterPro; IPR003623; IL6 MGF.
InterPro; IPR003573; IL6 MGF.GCSF.
Pfam; PF00489; IL6; 1.
PRINTS; PR00438; ICSE MGF.
PRODOM; PR008188; ICSE MGF.;
PROSITE; PS00254; INTERLEUKIN 6; 1.
CYCOKINE; Growth factor; Glycoprotein; 3D-structure.
DISULFID 65 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18858 MW; 28C26B24990C6DB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ^:
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                                                                                                                                                                                  -!- PTM: O-glycosylated.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
PDB; HBGD, 31-OCT-93.
PDB; 1BGE; 31-OCT-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.9%; Score 734; DB 1;
80.9%; Pred. No. 1.7e-60;
iive 11; Mismatches 22.
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                                                                                                                                                SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Secreted.
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Best Local Similarity 80.9°
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
175 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...ourled and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                  STRAIN=Holstein;
Heidari M., Kehrli M.E. Jr.;
Heidari M., Kehrli M.E. Jr.;
"Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte
colony stimulating factor.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 TPLGFARSLFQSFLLKCLEQVRKIQADGAELQERLCAAHKLCHPEELMLLRHSLGIFQAP
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InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6_MGF_GCSF.
PFEAM; PR00433; IL6GCSFMGF.
PRODOM; PD008388; GCSF MGF; 1.
SMART; SM00126; IL6; 1.
SWART; SM00126; IL6; 1.
CYCKINE; PS00254; INTERLEUKIN_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 195;
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                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PIM: 0-glycosylated.
-!- PIM: D-glycosylated.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
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TS -> RG
                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.7 ANGST. MEDLINE=94076341; PubMed=7504736
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195
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23
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CSF3 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                            Gloster S.E., Sandeman R.M., Strom A.D.G.,
"Cloning of a cDNA and gene encoding porcine granulocyte-colony
stimulating factor.",
Submitted (SEP-1997), to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
DIFFERSHITATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
CSF INDUCES GRANULOCYTES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .) (BY SIMILARITY)
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                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP
                           142 MEDLGAAPAVQPTQGAMPTFTSAFQRRAGGVLVASQLHRFLELAYRGLRYLAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.3%; Score 702; DB 1; Length 195; 79.2%; Pred. No. 1.7e-57;
                                                                                                                                               30-WAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Granulocyte colony-stimulating factor precursor (G-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
O-LINKED (GALNAC. . .) (BY :
A -> R (IN REF. 1).
W, 84787F20DB0AEAIC CRC64;
                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: O-glycosylated (By similarity).
-!- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART, SM01126, ILE, 1.
PROSITE, PS00254; INTERLEUKIN 6; 1.
Cytokine, Growth factor, Glycoprotein, Signal.
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                                                                                                            195
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InterPro; IPR003573; ILE MGF GCSF.
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123 A
21214 MW;
                                                                                                                  002837; 019180; 15-JUL-1998 (Rel. 36, Created) 30-MAY-2000 (Rel. 39, Last seq 28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00489; IL6; 1.
PRINTS; PR00433; IL6GCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, Y10494, CAA71518.1, -. EBMBL, U68482, AAB70701.1; -. EMBL, U68481; AAB70700.1; -. HSSP, P58813; 186C.
                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1997)
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57
85
154 1
123 1
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Kulmburg P.;
                                                                                                                                                                                                                     scrofa (Pig)
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Best Local Simi
Matches 137;
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CONFLICT
SEQUENCE
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                                                     SSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQM 121
                                                                                       83 SSCSSQALQLTGCINQLHGGLVLYQGLLQALAGISPELAPALDILQLDVTDLATNIWLQM 142
                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eur. J. Biochem. 165;7-12(1987).
-!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
CSF INDUCES GRANULOCYTES.
GRANULOCYTE COLONY-STIMULATING FACTOR.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsuchiya M., Asano S., Kaziro Y., Nagata S.;
"Isolation and characterization of the cDNA for murine granulocyte
                                                                                                                         EELGMAPALOPTOGAMPAFASAFORRAGGVLVASHLOSFLEVSYRVLRHLAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87190474; PubMed=3494605;
Tsuchiya M., Kaziro Y., Nagata S.;
"The chromosomal gene structure for murine granulocyte colony-
                                                                                                                                                                                                                                                                                                                                               (G-CSF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colony-stimulating factor.";
Proc. Natl. Acad. Sci. U.S.A. 83:7633-7637(1986).
                                                                                                                                                                                                                                                                                  01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Granulocyte colony-stimulating factor precursor
CSF3 OR CSFG.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: O-glycosylated (By similarity). SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00489; IL6; 1.
PRINTS; PR00433; IL6GCSFMGF.
ProDom; PD008388; GCSF MGF; 1.
SMART; SM0126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
CYLCKINE; Growth factor; Glycoprotein; Signal.
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                                                                                                                                                                                                                                                     208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Monomer.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P09919; IRHG.
MGD; MGI: MGI: GEF3.
InterPro; IPR003629; GGSF_MGF.
InterPro; IPR033573; ILG_MGF_GGSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=87017003; PubMed=3489940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M13926; AAA37672.1; -. EMBL; X05402; CAA28986.1; -.
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A29536; A26496.
HSSP; P09919; 1RHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                     MOUSE
                                                                                                                           122
                                                   62
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Gaps

;

25; Indels

Mismatches

11;

Conservative

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Similarity

PLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPL 61

FT

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ProDom; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            P26893; Q95KN6;
                                                                                                                                                                                     67;
                                                                                          DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                         36
                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                  PIG
                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol.
                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                     IL6_PIG
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    SETTTTTT
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                                                                                 ó
                                                                                                                                                             63 SCPSOALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQME 122
                                                                                                                                                                              62
                                                                                                                                    98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOI. Cell. Biol. 12:1728-1735 (1992).
-!- FUNCTION: HEMATOPOIETIC GROWTH FACTOR THAT STIMULATES THE PROLIFERATION HEMATOPOIETIC GROWTH FACTOR THAT STIMULATES THE PROLIFERATION AND COLONY FORMATION OF NORMAL AND TRANSFORMED AVIAN CELLS OF THE MYELOID LINEAGE.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                          3 LGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPBELVLLGHSLGIPWAPLS
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CMGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               β
                  (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=92195319; PubMed=1549124;
MEDLINE=92195319; PubMed=1549124;
MEDLINE=92195319; PubMed=1549124;
Sterneck E., Blattner C., Graf T., Leutz A.;
"Structure of the chicken myelomonocytic growth factor gene and "Structure of the chicken myelomonocytic cells specific activation of its promoter in avian myelomonocytic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE-89231616; PubMed=2785450; Mess B., Frank R., Leutz A., Damm K., Sterneck E., Kowenz E., Ness S., Frank R., Gausepohl H., Pan Y.-C.E., Smart J., Hayman M., Graf T.; molecular cloning of the chicken myelomonocytic growth factor reveals relationship to interleukin 6 and granulocyte colony
                                                                                    ..
o
                                                                                                                                                                                                                                 123 ELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLA
                                                         Length 208;
                                                      71.5%; Score 641; DB 1; Length 20 clarity 75.9%; Pred. No. 7.3e-52; Conservative 9; Mismatches 32; Indels
     110 BY SIMILARITY.
169 O-LINKED (GALNAC. . .) (B)
22421 MW; 0BF3622135C906DB CRC64;
                                                                                                                                                                                                                                                                                                                                       01-JAN 1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
08-FBB-2003 (Rel. 41, Last annotation update)
Myelomonocytic growth factor precursor (MGF).
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                               201 AA
                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6 MGF GCSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M85034; AAA48694.1; -. EMBL; X14477; CAA32639.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00489; IL6; 1.
PRINTS; PR00433; IL6GCSFMGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stimulating factor.";
EMBO J. 8:175-181(1989).
                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A42247; A42247.
HSSP; P35834; 1BGD.
       100 1
169 1
208 AA;
                                                           Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                  MGF CHICK
        DISULFID
                      CARBOHYD
                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                              P13854;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus
                                                                                                                                                                                                                                                                                        JLT 8
CHICK
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                                                                                                                                                                                                                                                                                                                         71 LAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPAL 130
                                                                                                                                                                                                                                                                                                                                                          96 AEVCFTQIRAGLHAYHDSLGAVLRLLPNHTTLVETLQLDAANLSSNIQQQMEDLGLDTVT 155
                                                                                                                                                                                                                                                                                        95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu S., Meng M., Gao R.; "Cloning and expression of interleukin 6 gene from Landrance \kappa Meishan
                                                                                                                                                                                                                                                                             11 QSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQ
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
Sus.
                                                                                   BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

, 240A8DD21B4244E6 CRC64;
                                                                                                                                                                                                                        2;
                                                                                                                                                                                      Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92360284; PubMed=1497880;
Mathialagan N., Bixby J.A., Roberts M.R.;
"Expression of interleukin-6 in porcine, ovine, and bovine
                                                                                                                                                                                                                                                                                                                                                                                              131 OPTO--GAMPAPASAFORRAGGVLVASHLOSFLEVSYRVLRHLAQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                    MYELOMONOCYTIC GROWTH FACTOR
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
NCBL_TaxID=9623,
                                                                                                                                                                                        33.9%; Score 304; DB 1; 40.6%; Pred. No. 6.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AA
                                                                                                                                                                                                                            28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Landrace x Meishan; TISSUE=Blood;
SMART; SM0126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
Growth factor; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reprod. Dev. 32:324-330(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterleukin-6 precursor (IL-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preîmplantation conceptuses.";
                                                                                                                                                          22373 MW;
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                     201
67
99
123
137
                                                                                                                                                          201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scrofa (Pig)
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SIMILARITY: Belongs to the IL-6 superfamily.
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22
64
93
164
205 AA;
                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                               49
                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
  음
                                                                                                                                                                                                                                                                                                                                                                                                       원
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          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   KTEELIKYILGKISAMRKEMCEKYEKCENSKEVLAENNLNLPKWAEKDGCFOSGFNOETC 111
                                                                                                                                                                                                                                                                                                                                                                        75 LSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPT- 133
                                                                                                                                                                                                                                                                                                                                                                                          LMRITTGLVEFÖIYLDYLÖKBYESNKGNVEAVÖISTKALIQTLRÖKGKNPDKÄTTPNPTT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ōrcinus orca (Killer whale).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Odontoceti, Delphinidae,
restrictions on
                                                                                                                                                                                                                                                                                                                               16 KCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP-WAPLSSCPSQALQLAGC
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                            ŝ
                                                                                                                                                                                                                                                                                      Score 106.5; DB 1; Length 212; Pred. No. 0.0098;
                                                                                                                                                                                                    Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                BY SIMILARITY.

BY SIMILARITY.

E -> G (IN REF. 1).

1E736FB230B4FC5D CRC64;
 There are no
                                                                                                                                                                                                                                                                                                                                                                                                                  134 -OGAMPAFAS--AFQRRAGGVLVASHLQSFLEVSYRVLR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                      210
                                                                                                                                                                                                                                                                                                          85;
                                                                                                                                                                                                                                                                                                                                                                                                                                | : | : | : | : | : | INAGLIDKLOSQNEWKKNTKIILILRSLEDFLOFSLRAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-FBB-2003 (Rel. 41, Last annotation update)
Interleukin-6 precursor (IL-6) (Fragment).
                                                                                                                     InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
PRIMIX; PR00439; IL6, 1.
PRODOM; PD004356; Interleukin_6; 1.
SWART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
Acute phase; Oylokine; Growth Factor; Glycop; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 AA
                                                                                                                                                                                                                                                                                                          Mismatches
 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=96163018; PubMed=8575817;
                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                      30 212 IN
72 78 BY
101 111 BY
30 30 E
212 AA; 23952 MW;
                                                           EMBL, M86722; AAC37333.1; -.
EMBL, M80258; AAC27127.1; -.
EMBL, AF309651; AAC27730.1; -.
PIR, I46590; 146590.
PIR, 146621; 146621.
HSSP, P05231; 1ALU.
                                                                                                                                                                                                                                                                                     11.9%;
22.6%;
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9733;
                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL6_ORCOR
Q28747;
                                                                                                                                                                                                                                DISULFID
DISULFID
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                           112
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                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL6_ORCOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 SGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGA--- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 VRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP-WAPLSSCPSQALQLAGCLSQLH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKY ILGKI SAMRKEMCEKYDKCENSKEALAENNINL PKMAEKDGCFQSGFNQETCLMRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
NCBL_TaxID=9796,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
9
                                                                                                                                                                                                                                       DB 1; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., "Molecular cloning of equine interleukin-6."; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         equine
                                                                                                                                                                                                                                                                                                                                                                                                                                           -LINKED (GLCNAC. . .) (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=2059380; PubMed=11137120;
Swiderski C.E., Sobol G., Lunn D.P., Horohov D.W.;
"Molecular cloning, sequencing, and expression of e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --MPAFASAFQRRAGGVLVASHLQSFLEVSYRVLR 169
                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 101; DB 1; Pred. No. 0.03; 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 NNLQSQNDDWMKNTKIILILRSLENFLQFSLRAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jet. Immunol. Immunopathol. 77:213-220(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
                                                                                                                                                  EMBL; L46803; AAB01429.1; -.
HSSP; P05231; 1ALU.
InterPro; IPR003573; IL6_MGF_GCSF..
InterPro; IPR003574; Interleukin_6.
Pfam; PP00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL6_HORSE
Q95181; O19007; O46568;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last seq
10-ACT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                        23266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-6 precursor (IL-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%;
20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Conservative
                                                                                                                                                                                                                                                                                                                                                            205
205
70
103
164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Lai A.C.K.;
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153 VASHLQSFLEVSYRVLR 169
                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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    SOLUTION OF THE TEATH THE PERSON OF THE PERS
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                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMAEKDGCFQSGFNQETCLMKITTGLSEFQIYLEYLQNEFKGEKENIKTMQISTKVLVQI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and expression of equine interleukin-6.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation,
hepatocytes it induces acute phase reactants (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PLGPASSLPQSFLL---KCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 -WAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 IWQQMEELGMA---PALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        řelis silvestris catus (Cat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Felidae, Felis.
NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 21.6%; Pred. No. 0.038;
Matches 38; Conservative 35; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A62F4C234056BF66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
INTERLEUKIN-6.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (F.
N-LINKED (GLCNAC. ..) (F.
LS -> FF (IN REF. 1).
T -> A (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T -> A (IN REF. 3)
I -> V (IN REF. 2)
V -> I (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23325 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interleukin-6 precursor (IL-6)
                                                                                                                                                                                                                                                                                                                                                                          EMBL; U64794; AAB87703.1; -.
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CARBOHYD
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P41683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
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                                                                                                                                                                                                                                                                                                                                                       Proc. Soc. Exp. Biol. Med. 204:301-305 (1993)
-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
-!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
happrocytes it induces acute phase reactants.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the IL-6 superfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> LSCSHRRVAEAHNN (IN
                                                                                                                                                                                                             TISSUE=Lymphocytes;

BrabLine=2465249; PubMed=8234373;
Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;

Molecular cloning and characterization of a cDNA encoding feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inter...

( InterPro) IPRUJE; 1.

R PÉAN; PRO0489; IL6; 1.

JR PRINTS; PR00433; IL6GCSFWGF.

DR PRODITS; PR00254; INTERLEUKIN_6; 1.

DR SWART; SM00126; Inte; 1.

DR PROSITE; PS00254; INTERLEUKIN 6; 1.

FT SIGNAL

T SIGNAL

28 208

T SIGNAL

PT CHAIN

FT CHAIN

97 107 BY SIMILARITY.

1 -> N (IN REF. 2).

1 -> P (IN REF. 2).

1 -> P (IN REF. 2).
                   Ohashi T., Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,
Hasegawa A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.6%; Score 95; DB 1; Length 208; 23.9%; Pred. No. 0.11; tive 30; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
INTERLEUKIN-6.
BY SIMILARITY.
BY SIMILARITY.
T -> N (IN REF. 2).
E -> K (IN REF. 2).
AKLQSQEEWLRHTTI -> LSCSHRRV.
REF. 2).
RSF. 2).
RSF. 2).
RSF. 2).
RSF. 2).
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                                                                                "Molecular cloning of feline interleukin-6 cDNA."; J. Vet. Med. Sci. 55:941-944(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 116914; AAA16620.1; -.
EMBL; D13227; BAA02507.1; -.
PIR; 146084; 146084.
HSSP; P05231; 1116.
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
MEDLINE=94162386; PubMed=8117820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23401 MW;
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Best Local Similarity 23.9'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 AA;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    interleukin-6.";
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RC STRAIN=Berkeley;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., R.A Adams M.D., Celniker S.E., Holt R.A., Shiburner M., Henderson S.N., Gotorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., R.A. Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D., Man K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D., R.A. Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M., Ballow R.M., Bauch A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballow R.M., Bauch M.R., Bouck J., Stoketein P., Brothard I., R. Burtis K.C., Butman D.A., Putler H., Cadieu S., Center A., Chadra I., R.A. Cawley S., Dahlke C., Dayraktaroglu L., Belbiakov S., Burtis K.C., Busam D.A., Abuller H., Cadieu S., Center A., Chadra I., R.A. Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P., Botsh M., Cawley S., Dahlke C., Dayraktaroglu L., Belbiakov S., Balli M., Kony E., Downes M., Dagan-Rocha S., Dunkov B.C., Dunn P., Roder C., Gabrielista C.C., Ferraz C., Ferraz C., Ferraz G., Cabrielia A.E., Garg N.S., Gelbart W.M., Glasser K., Alaria M., Kalush F., Karpen G.H., Ke.Z., Kennison J.A., Ketchnu K.A., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Lin X., Mattei B., McInton C., Mories M., Mosherei A., Moyley M., Murphy B., Murphy L., Mursh, W. McPherson D.L., Melson D.R., Mattei B., McInton K.A., Musch K., Dilard J., Puri W., Sanith T., Shen E., Shen H., Shen E., Shen H., Shen E., Shen H., Wang X., Wallams S.M., Woodage T., Stampson M., Strong K., Wasaarnan D.A., Wainstock G., Scheeler F., Shen H., Shung X., Wallams S.M., Woodage T., Stampson M., Strong S., Zho O., Shen S., Shen Z., Shen S., Shen Z., Shen S., Shen S., Shen S., Shen Z., Shen S., Walliams S.M., Woodage T., Stampson M., Strong S., Zho O., Shen S., Shen S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:2185-2195(2000).
-!- FUNCTION: Regulator of cell fate decisions in multiple lineages.
Specifically, functions as a determination factor that specifies sensory organ identity in precursor cells. Probably also involved in cell type specification of Malpighian tubules. In absence of cut gene external sensory organs are transformed into chordotonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88232956; PubMed=2897632;
Blochlinger K., Bodmer R., Jack J., Jan L.Y., Jan Y.N.;
"Primary structure and expression of a product from cut, a locu
involved in specifying sensory organ identity in Drosophila.";
Nature 333:629-635(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, brosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                               HNCU_DROME STANDARD; PRT; 2175 AA. P10160, O9W3O6; PNT; 10, Created) O1-MAR-1989 (Rel. 10, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) CT OR CG11387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
190 TLRRLEDFLQFSLRAVR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1438 GLASKWQAASLPMQKWMSELKLQEPAQAQHLMQQWQAAAMSAAMQQQQ-----VAQAQQQ 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 GLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 DGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLSQLHSGLFLYQ 86
TISSUE SPECIFICITY: Detected in many cells in the central nervous system, all external sensory organs, some peripheral neurons, and in the non-neural cells of the spiracles and the Malpighian
                                                            DEVELOPMENTAL STAGE: Cell-specific pattern of expression. Broadly
                                                                        expressed during embryonic development.

DOMAIN: Asn at position 47 of the homeobox may participate regulating DNA-binding activity by promoting homo- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.0%; Score 89.5; DB 1; Length 2175;
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Nuclear protein; Repeat; Coiled coi

Nuclear Drotein; Repeat; Coiled coi

OILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

COUT 2.

CUT 2.

CUT 2.

CUT 3.

ALA/GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08BF80C4861BD0AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALA-RICH
HIS/GLN-RICH (OPA-REPEAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALAYOLU.
ALA-RICH.
ASP/GLU-RICH (ACIDIC).
ASN-RICH.
ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                  EMBL; X07985; CAA30794.1; -.
EMBL; AE003441; AAF46264.2; -.
PIR; SO3170; S03170.
TRANSPS; TO2004; -.
FlyBase; FBGN0004198; ct.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:000587; P:wing margin morphogenesis; NAS.
InterPro; IPR003350; Hmoeo CUT.
InterPro; IPR003350; Hmoeobox;
Pfam; PF02376; CUT; 3.
Pfam; PF02376; CUT; 3.
Probom; PD00010; Homeobox; 1.
Probom; PD00010; Homeobox; 1.
                                                                                                                   heterodimerization.
SIMILARITY: Belongs to the CUT homeobox family.
SIMILARITY: Contains 1 homeobox domain.
SIMILARITY: Contains 3 CUT domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALA-RICH.
ASP/GLU-RICH (ACIDIC).
ALA/PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
Transcription regulation; Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
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2175 AA;
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DOMAIN
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DOMAIN
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DOMAIN
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Matches
셤
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147 RAGGVLVASHLQSFLEVSYRVLRHLAQ 173

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SUBCELLULAR LOCATION: Nuclear (Probable).

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151 IQILKQKIADLITTPATNTDLLEKMQSSNEWVKNAKIILLILRNLENFLQFSLRAIR 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 22.0
                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9720;
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69
98
                                                                                                                                                                                116 PHOVI
Q28819;
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Matches
                                                                                                                 RESULT 15
IL6_PHOVI
                                                                                                                                                                                                                    SOLUTION NO DEPT TO THE PROPERTY OF THE PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 PLGEDFKNDTTPGRLLLTTPEKTEALIKRMVDKISAMRKEICEKNDECESSKETLAENKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTIWOOMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Wakaryota: Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL)
A0F000B9BA2EC341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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InterPro; IRR0025...
Plan; PRO0483; IL6GCSFMGF.
R ProDom; PD004336; Interleukin_6; 1.
R RMART; SM00126; IL6; 1.
DR RROSITE; PS00254; INTERLEUKIN 6; 1.
RWA Acute phase; Cytokine; Growth factor; Glycoprote signal and some signal and so
                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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37; Mismatches
              |||| : : |||| 1493 AQQAQQHLQQQAQHLAQ 1519
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InterPro; 1FPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PP00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Holstein;
MEDLINE-93076003; PubMed-1446077;
                                                                                                                                                                                                                                                                                                                                                                                                        nterleukin-6 precursor (IL-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 N
23758 MW;
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                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR, A56610; A56610.
HSSP; P05231; 11L6.
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38
208 AA;
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Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                   L6 BOVIN
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=96163018; PubMed=8575817;

MEDINE=96163018; PubMed=8575817;

King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,

King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,

A stott J.L., Ferrick D.A.;

Molecular cloning and sequencing of interleukin 6 cDNA fragments from

"Molecular cloning and sequencing of interleukin 6 cDNA fragments from

"Molecular cloning and sequencing of interleukin 6 cDNA fragments from

"Molecular cloning and sequencing interior are sequencing in memogenetics 43:190-195(1996).";

Immunogenetics 43:190-195(1996).

"Immunogenetics 43:190-195(1996).";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 KCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP-WAPLSSCPSQALQLAGC
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                                                                                                                                                                                                                                                                                                                                                               Phoca vitulina (Harbor seal).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
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PROD0435, ILGGCSFMGF.
SMART; SM00126, IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
Acute phase; Cytokine; Growth factor; Glycoprotein; Signal.
NON TER
<1 26 BY SIMILARITY.
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INTERLEUKIN-6.
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W; 75144922843B48E9 CRC64;
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                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Interleukin-6 precursor (IL-6) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.4%; Score 84.5; DB
22.0%; Pred. No. 1;
:ive 30; Mismatches
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209
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HSSP; P05231; IL6.
InterPro; IPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
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Search completed: October 6, 2004, 16:04:29 Job time : 25 secs

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October 6, 2004, 15:58:27; Search time 117 Seconds (without alignments) 469.232 Million cell updates/sec
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896
1 TPLGPASSLPQSFLLKCLEQ.....SHLQSFLEVSYRVLRHLAQP 174
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                              OM protein - protein search, using sw model
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1: Sp archea:*
2: Sp_bacteria:*
3: Sp_lungi:*
4: Sp_lungi:*
5: Sp_lungi:*
5: Sp_lungi:*
5: Sp_manmal:*
5: Sp_man
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Gapop 10.0 , .Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_plant: *

sp_rvirus:* sp_bacteriap:*

sp_archeap:*

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	Description	Q8n4w3 homo sapien	O9gjuO felis silve	P97712 rattus norv	Q8mke0 equus cabal	Q90yi0 gallus gall	Q8mj75 sus scrofa	Q9xt80 delphinapte	Q9h2a5 homo sapien	Q8d706 vibrio vuln	Q9kt16 vibrio chol	Q9npf7 homo sapien	Q8mke5 sus scrofa	Q9a523 caulobacter	Q9i019 pseudomonas	Q8rjy3 stigmatella	Q34008 beta vulgar
SUMMARIES	ΩI	QBN4W3	00 c 360	P97712	Q8MKE0	01X06Ö	Q8MJ75	Q9XTB0	Q9H2A5	980706	Q9KTL6	Q9NPF7	QBMKES	Q9A523	61016	OBRJY3	Q34008
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	Score	968	744	634	511	111	110.5	108	96	94.5	94	63	89.5	88.5	88.5	88.5	86
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mus	Q7tq21 mus musculu	Qacfae mus musculu	o	Q865w7 camelus bac	Q8lqr8 oryza sativ	Q9n2h9 sus scrofa			Q9tth3 aotus lemur	O29363 archaeoglob	Q9p0s7 homo sapien	Q8zth1 pyrobaculum	Q8mkh0 saimiri sci	Q923k8 cavia porce	Q8chl9 cavia porce	O	Ø	Q7zty0 brachydanio		Q83vsl pseudomonas	094927 homo sapien	O33956 streptomyce	oryza		Q9rxx9 deinococcus	Q9nt11 homo sapien	Q8dg52 synechococc	Q8ndg1 homo sapien
Q8CF87	Q7TQ21	QBCF88	Q811T9	Q865W7	Q8LQR8	Q9N2H9	Q865X6	Q9TTH4	Q9TTH3	029363	Q9P0S7	Q8ZTH1	Q8MKH0	Q923KB	Q8CHL9	Q9MYZ7	Q28403	Q7ZTY0	Q8GMH8	Q83VS1	094927	033956	Q9AV51	Q7XDB0	Q9RXX9	Q9NT11	Q8DG52	Q8NDG1
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ALIGNMENTS

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		PRT; 200 AA.	Created)	Last sequence update)	Last annotation update)			Craniata; Vertebrata; E	; Catarrhini; Hominidae; Homo.				EMBL/GenBank/DDBJ databases.		lar; IEA.	Figrowth factor activity; IEA.	ponse; IEA.	É.	GCSF.			· rd			; 8648AA55B329A96C CRC64;	006. DB 4. Length 200.	Score 850; DB 4; Dength 200; Pred. No. 1.98-77;		TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAP 6	THE SECOND SECON	
		PRELIMINARY;	(TrEMBLrel, 22.	(TrEMBLrel, 22,	(TrEMBLrel. 24,	al protein.	(Human)		Butheria; Primates;	=9606;	ROM N.A.	n;	 -2002) to the	AAH33245.1;			6955; P:immune response;	InterPro; IPR003629; GCSF_MGF.	IPR003573; IL6 MGF	Pfam; PF00489; IL6; 1.	00433; IL6GCSFMGF.	ProDom; PD008388; GCSF_MGF; 1	SMART; SM00126; IL6; 1.	SOUSS4; INTEREBURE	200 AA; 21543 MW;		100.0%; milarity 100.0%;	vative	PLGPASSLPOSFLLKCLE		
RESULT 1	N 4 N	ID Q8N4W3			DT 01-JUN-2003	DE Hypothetical	OS Homo sapiens	OC Eukaryota; Metazoa;	OC Mammalia; Eutheria;	OX NCBI_TaxID=9606;		RC TISSUE=Skin;	RL Submitted (DR EMBL; BC033245;	_		DR GO; GO:0006955;	DR InterPro; I		DR Pfam; PF004	DR PRINTS; PR00433;			UK FRUSIIE; FSUC		40 10 10 10 10 10 10 10 10 10 10 10 10 10	Query March Best Local Sim	Matches 174; Conser	Qy 1 TE	=i	

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LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALBGISPELGPTLDTLQLDVADFATTIWQQ 120
                                                 LSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LSSCPSQALQLAGGLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 LSSCSSQALQLTGCLRQLHSGLFLYQGLLQALAGISPELAPTLDMLQLDITDFAINIWQQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TPLGPASSIPQSFLIKCLEQVRKIQGDGAALQEKLCATYKLCHPBELVLLGHSLGIPWAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 TPLGPTSSLPQSFLLKCLEQVRKVQADGTALQERLCAAHKLCHPEELVLLGHALGIPQAP 81
                                                                                                                                         MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 200
                                                                                                         MEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Yamamoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K., Saito Saito Sajimento H., Hasegawa A., Ueda S.,
Tsujimcto H., Hasegawa A., Ueda S.,
"Molecular cloning and expression of the cDNA encoding feline granulocyte colony-stimulating factor.",
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB042552; BAB17799.1; --
EMBL; AB042553; BAB17757.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 195;
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Best Local Similarity 81.0%; Pred. No. 5.7e-63;
Matches 141; Conservative 11; Mismatches 22; Indels
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195 AA; 21255 MW; 544C682909412FCF CRC64;
                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
Granulocyte colony-stimulating factor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; IEA.
GO; GO:000515; F:growth factor activity; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                      195 AA
                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00254; INTERLEUKIN 6; 1.
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InterPro; IPR003573; IL6_MGF_GGSF.
Pfam; PF00489; ILf6; 1.
PrNTGS; PR00433; IL6GCSFMGF.
Probom; PD008388; GGSF_MGF; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LGPASSIPQSFILKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLS
                                                                                                                                           Eukaryote; Metazoa; "Chyrdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                  MEDILNE-27074655; PubMed-8917083; MEDILNE-27074655; PubMed-8917083; MATOLINE-270774655; PubMed-8917083; MCIONING and expression of the cDNA encoding rat granulocyte colony-stimulating factor."; Gene 175:101-104(1986). EMBL: U37101-104(1985). FMBL: U3701-104(1985). HSSP; P09919; 1RHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 ELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLAQP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00433; IL6GCSFWGF.
ProDom; PD008388; GCSF_MGF; 1.
SWART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
SEQUENCE 214 AA, 23659 WW; 29EB88B17B684C55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Granulocyte colony-stimulating factor.
                                                                Last sequence update)
Last annotation update)
                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0008083; F:growth factor activity; IEA.
GO; GO:0006955; P:immune response; IEA.
214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AA
                                                                                                    Granulocyte colony stimulating factor. Rattus norvegicus (Rat).
                                           (TrEMBLrel. 03, Created)
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003629; GCSF MGF.
InterPro; IPR003573; IL6 MGF GCSF.
Pfam; PF00489; IL6; 1.
                                      01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-JUN-2003 (TrEMBLrel. 24,
PRELIMINARY;
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                         NCBI_TaxID=10116;
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657F8049F25BD2F8 CRC64;
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                                                                                                                                                                                                   153 ---VASHL----QSFLEVSYRVLRHL 171
                                                                                                                                                                                                                207 IEKITMHLILRDFTSFMEKTVRAVRYL 233
    26790 MW;
                                                                                                                                                                                                                                                                                        Q8MJ75;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                              PRELIMINARY;
   241 AA;
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Best Local Similarity
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    SEQUENCE
                         Query Match
Best Local S
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Matches
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Q8MJ75
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Q9XT80
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                                                                                                                                             48 VILGHSLGIPWAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQ 107
                                                                                                                                                                                        LDVADFATTIWOOMEELGMAPALOPTQGAMPAFASAFORRAGGVLVASHLQSFLEVSYRV 167
                                                                                                                                                                                                      61 LDVTDFATNIWQQMEDLGVAPVVQPTHGPMPTFASAFQRRAGGVLVASNLQRFLELAYRG 120
                                                                                                                                                                  9
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves; Neognathae, Galliformes; Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schneider K., Klaas R., Kaspers B., Staeheli P.;
-chicken interleukin-6: cDNA structure and biological properties.";
Submitted (FBB-2001) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,

Wigley P.;

"Differential cytokine expression in avian cells in response to
invasion by Salmonella typhimurium, Salmonella enteritidis and
Salmonella gallinarum.";

Microbiology 146:3217-3226 (2000).
                                                                                                                        ..
                                                                                                 Query Match 57.0%; Score 511; DB 6; Length 127; Best Local Similarity 79.5%; Pred. No. 5.5e-41; Matches 101; Conservative 9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaiser P.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ309540; CAC40812.1;
GO; GO:0005576; Cactacallular; IEA.
GO; GO:0005125; F:cytockine activity; IEA.
GO; GO:0005139; F:interleukin-6 receptor binding; IEA.
GO; GO:0005139; F:interleukin-6 receptor binding; IEA.
InterPro; IPR003573; IL6_MGF_GCSF.
InterPro; IPR003574; Interleukin-6.
Last sequence update)
Last annotation update)
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MATURE CHIL-6.
                                                                                                                                                                                                                                                                                                                                  Created)
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PRINTS; PR00433; IL6GCSFNGF.
ProDom; PD004356; Interleukin 6; 1.
SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                 Interleukin-6 precursor
                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken)
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|121 LRYLAEP 127
                                                                                                                                                                                                                                  LRHLAOP 174
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SIGNAL
CHAIN
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157 EKQNVESLCYSTKHLAATİRQMV-----INPDEVVIP--DSAAQKSLLANLKSDKDW 206
                                                                                                                               75 LSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPT- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 PEELVILGHSLGIPWAPLSSCPSOALQLAG-----CLSQLHSGLFLYQGLLQALEGISPE
                                                                                                                                                                                                                                                                                                                                                                               99 LGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVL----
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                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                  52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 12.3%; Score 110.5; DB 6; Length 212; 1 Similarity 23.3%; Pred. No. 0.015; 37; Conservative 32; Mismatches 85; Indels 5
ch 12.4%; Score 111; DB 13; Length 241; Similarity 22.2%; Pred. No. 0.015; 46; Conservative 35; Mismatches 74; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Lee D., Yoo H., Choi I.;

Lee D., Yoo H., Choi I.;

Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF518322; AAM74938.1; --

GO GO:0005576; C:extracellular; IEA.

GO; GO:0005125; F:cytokine activity; IEA.

GO; GO:0005125; F:interleukin-6 receptor binding; IEA.

GO; GO:000518; F:interleukin-6 receptor binding; IEA.

InterPro; IPR003574; ILG MGF GCSF.

InterPro; IPR003574; Interleukin-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRINTS; PRO143; ILGGCSFMGF.
ProDom; PD004356; Interleukin_6; 1.
SMART; SM0126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
SROUBNCE 212 AA, 23881 MW; IF540E7030BCFD77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 NAGLLDKLOSONEWMKOTKIILILRSLEDFLQFSLRAIR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QGAMPAFAS -- AFQRRAGGVLVASHLQSFLEVSYRVLR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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9

Gaps

40;

Indels

77;

DB 4; Length 189;

-----SIG 55

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56 IPWAPL-SSCPSQALQ--LAGCLSQLHSGLFLYQGLL--QALEGISPELGPTLDTLQLDV 110
                                                                                                                                                                                               68 VPHIQCGDGCDPQGLRDNSQFCLQRIHQGLIFYEKLLGSDIFTG-EPSLLPDSPVAQLHA 126
                                                                                                                                                                                                                                                              127 SILGISQILQPEGHHWETQQIPSLSPSQ-----PWQRLILRFKILRSLQAFVAVAAR 178
                                                                                                                                   LLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHP----LVGHMDLREEGDEETTND 67
                                                                                                                                                                                                                                   111 ADFATTIWQQME----ELGWAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYR
                                                                                                        14 LLKCLEQVRKIQGDGA-----ALQEKLCATYKLCHPEELVLLGH--
HGNC:15488; IL23A.
E 189 AA; 20744 MW; BFB5C0F42D4C1E3A CRC64;
                                      10.7%; Score 96; DB 4;
ilarity 26.1%; Pred. No. 0.31;
Conservative 19; Mismatches
                                                          Local Similarity
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SEQUENCE 455 AA
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                                                                                                                                                                                                                                                                                                                                 179
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                SEQUENCE
                                               Query Match
   Genew;
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                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGA--- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGLLEYQIYLDYLQNEYEGDKGSIEAVQISIKALAQILRQKVKNPDEVTTPDPTTNASLM 171
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Rastelein R.A.,
"Novel pl9 Protein Engages IL-12p40 to Form a Cytokine, IL-23, with Biological Activities Similar as Well as Distinct from IL-12.";
EMBL, AF301620; AAG37232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 VRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIP-WAPLSSCPSQALQLAGCLSQLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                Delphinapterus leucas (Beluga whale).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
Monodontidae; Delphinapterus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human). Substructions (Brandara, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 9
                                                                                                                                                                                          SEQUENCE FROM N.A.
St-Laurent G., De Guise S., Fournier M., Archambault D.,
St-Laurent G., De Guise S., Fournier M., Archambault D.,
Molecular cloning and phylogenetic analysis of beluga whale
(Delphinapterus leucas) interleukin 6.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, APO76643;
APA42929.1;
HSSP; P05231; 1ALU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.1%; Score 108; DB 6; Length 208; Best Local Similarity 21.3%; Pred. No. 0.025; Matches 33; Conservative 35; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SMO0126; IL6; 1.
PROSITE; PS00254; INTERLUKIN_6; 1.
SEQUENCE 208 AA, 23456 MW; BICCBSCGE80389C4 CRC64;
                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukhn-6 receptor binding; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR003573; IL6 MGF GCSF.
InterPro; IPR003574; Interleukin_6.
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01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Interleukin 23 p19 subunit.
                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 --MPAFASAFQRRAGGVLVASHLQSFLEVSYRVLR 169
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   208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00433; ILGGCSFMGF.
ProDom; PD004356; Interleukin_6; 1.
SMART; SM00126; IL6; 1.
   PRT;
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     PRELIMINARY;
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Q9H2A5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SLGIPWAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PEGAPTLDT
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                                                                                                                                                                                                                                                                                  STEAIN=CMCP6;
Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB016809; AA007321.1;
GO; GO:00168020; C:membrane; IEA.
GO; GO:0016805; F:protein transporter activity; IEA.
GO; GO:0008810; P:transport; IEA.
InterPro; IFR02898; MotA. ExbB.
Pfam; PF01618; MotA. ExbB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 AA; 49446 MW; 241A87B1CDB8E942 CRC64;
                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
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24.6%; Pred. No. 1.2;
tive 15; Mismatches
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455 AA
PRT;
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                                                                                                        Biopolymer transport protein.
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  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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ID Q9KTL6
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LLKCLEQVRKIQGDGA-----ALQEKLCATYKLCHPBELVLLGH-----SLG 55
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Submitted (MAR-2002) to the EMBL/GenBank/DDE
EMBL; AF493992; AAM27192.1; ...
GO; GO:000576; C:extracellular; IEA.
GO; GO:0005125; F:cytokine activity; IEA.
GO; GO:0005138; F:interleukin-6 receptor
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR003574; Interleukin_6.
Pfam; PF00489; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          999
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01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 VLRH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 VFAH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 GA 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Q9A523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 ASDPDLFLLAAL--VRALAGAPANILDATCDAILASPAICHPEVLIALA---GRSWMSLE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 SSLPQSFLLKCLEQVRKIQGDGAALQEKLC----ATYKLCHPEELVLLGHSLGIPWAPLS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 S---CPSQALQLAGCLSQ-LHSGLFLYQGLLQALBGI-----SPELGPTLDTLQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINEL TOT NIG661 / Serotype 01,
MEDLINE=20406833; Pubbled=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Ralzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.5%; Score 94; DB 16; Length 345;
Best Local Similarity 32.2%; Pred. No. 0.97;
Matches 38; Conservative 15; Mismatches 43; Indels 3
                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.4%; Score 93; DB 4; Length 189; ilarity 26.1%; Pred. No. 0.59; Conservative 19; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Spleen;
Hirata Y., Kosuge Y.;
Hirata Y., Kosuge Y.;

"SGRF; a novel member of the IL-6/G-CSF family.";

Submitted (UUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AB030000; BAA93686.1; -.

EMBL; AB030001; BAA93687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR, VC0886;
InterPro, IPRO01303; Aldolase II N.
Hypothetical protein; Complete proteome,
SEQUENCE 345 AA; 38781 MW; E446D7798ADA7E01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51B5C0F188EC1B9F CRC64;
        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypochetical protein VC0886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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189 SG
20730 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 406:477-483(2000).
EMBL, AE004172; AAF94048.1; -.
PIR, C82270; C82270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Cr
01-OCT-2000 (TrEMBLrel. 15, La
01-MAR-2003 (TrEMBLrel. 23, La
SGRF precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                             Vibrio.
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20
189 AA;
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             Vibrionaceae, Vi
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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SIGNAL
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75 LSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQ 134
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12 LIPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHP----LVGHMDLREEGDEETTND 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus
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ProDom; PD004356; Interleukin_6; 1.
SWART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN 6; 1.
SEQUENCE 214 AA; 23765 MW; 50849FB04D0BD7F CRC64;
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82 LFLYQGLLQALEGISPE------LGPTLDTLQLDVADFATTIWQQMEELGMA 127
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                                                                                                                                                               GO, GO:0016020; C:membrane; IEA.
GO; GO:0016020; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000574; F:DNA binding; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0010740; F:transferase activity; IEA.
GO; GO:000156; F:two-component response regulator activity; IEA.
GO; GO:000156; F:two-component sensor molecule activity; IEA.
GO; GO:000160; P:sensory perception; IEA.
GO; GO:000160; P:sensory perception; IEA.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003584; Bact sens pr C.
InterPro; IPR003661; His_Kinase.
InterPro; IPR003661; His_Kinase.
InterPro; IPR003661; His_Kina.
InterPro; IPR003661; His_Kina.
InterPro; IPR003661; His_Kina.
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Gaitatzis N., Silakowski B., Kunze B., Nordsiek G., Blocker H.,
Hofle G., Muller R.;
"The biosynthesis of the aromatic myxobacterial electron transport
inhibitor stigmatellin is directed by a novel type of modular
polyketide synthase.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ421825; CAD19088.1; -.
GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. .; IEA.
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Bysteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Cystobacteraceae; Stigmatella.
NCBI_TaxID=41;
-i- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
EMBL; AEO04709; AAG06212.1; -.
PIR; F83292; F83292.
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity
Matches 50; Conserv
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SEQUENCE 786 AA;
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C STRAIN=ATC 15620 / PAO1;

MEDLINE=20437337; Pubmed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., A Hickey M.d., Brinkman F.S.L., Hufnagle W.O. Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., A Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., A Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

T "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";

I opportunistic pathogen.";

I opportunistic Pathogen.";

I Nature 406:959-964 (2000)

I Nature 406:959-964 (2000)

I REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
                                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC 19089 / CB15;
STRAIN-ATCC 19089 / CB15;
MSDLINE-113698; PubMed-11259647;
MSDLINE-113698; PubMed-11259647;
Midrman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Elsen J., Heidelberg J.F., Newton R.S., Gaphens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 LGHSLGIPWAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 VADFATTIWQ-QMEELG------MAPALQP-TQGAMPAFASAFQRRAGG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            666 AA; 67569 MW; 1ED3FF286CA8B6C0 CRC64;
                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) 01igopeptide transporter, OPT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Probable sensor/response regulator hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.9%; Score 88.5; DB 16; 32.5%; Pred. No. 7.1;
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InterPro; IPR04813; Tetrpept_transpt.
Pfam; PF03169; OPT, I.
TIGRPAMs; TIGR00728; OPT sfam; 1.
TIGRPAMs; TIGR00733; TIGR00733; 1.
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                                                                                                                                                                               crescentus,
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Best Local Similarity
                                                                                                                                                                                                                                                                                       NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 666 AA;
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                                                                                                                                                                           Caulobacter
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Q91019; Q91019;

RESULT 14 Q91019

Matches

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DDT REPARED DE REPARED

10;

53; Gaps

81

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63 SCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQME 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
9.9%; Score 88.5; DB 2; Length 1931;
Best Local Similarity 25.3%; Pred. No. 25;
Matches 41; Conservative 24; Mismatches 48; Indels 49.
RGO; GO:0016740; F:transferase activity; IEA.

GO; GO:0006633; P:fetty acid biosynthesis; IEA.

GO; GO:0006633; P:fetty acid biosynthesis; IEA.

GO; GO:0006632; P:metabolism; IEA.

InterPro; IPR001272; Ac trans.

InterPro; IPR001601; Wethyltransf.

InterPro; IPR001601; Wethyltransf.

InterPro; IPR001613; Pb bind.

R InterPro; IPR00051; SAM bind.

R InterPro; IPR001515; Thiolase.

R Pfam; PF00498; Actoacyl-synt. 1.

R Pfam; PF00509; Actoacyl-synt. 2.

R Pfam; PF00501; Ketoacyl-synt. 1.

R Pfam; PF00501; Ketoacyl-synt. 2.

R Pfam; PF00506; B KETOACYL, SYNTHASE; 1.

R PROSITE; PS00066; B KETOACYL, SYNTHASE; 1.

R PROSITE; PS00099; THIOLASE].

R PROSITE; PS00099; THIOLASE].

R PROSITE; PS00099; THIOLASE].

R PROSITE; PS00099; THIOLASE].

R PROSITE; PS00099; THIOLASE].

R PROSICORE 1931 AA; 208260 MW; 6DBAA0F496A9A84F CRC64;
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Search completed: October 6, 2004, 16:06:34 Job time : 121 secs

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RESULT 1

US-08-104-445-2

Sequence 2, Application 08/104445

Sequence 2, Application 08/104445

Sequence 2, Application 08/104445

Sequence 2, Application 08/104445

Sequence 2, Application 08/104445

Sequence 2, Application 08/104445

APPLICANT: SCHOUSTER, ERWIN

APPLICANT: SCHOUSTER, ERWIN

TILLE OF INVENTION: BACTERIAL XYLANASE, METHOD FOR ITS

TILLE OF INVENTION: BACODING A XYLANASE, DNA FRAGMENT,

TILLE OF INVENTION: BACODING A XYLANASE, DNA FRAGMENT,

TILLE OF INVENTION: BACODING A XYLANASE, AND METHOD FO

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Azlington

STATE: Virginia

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
SECTIVE TO STEEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: 08/104,445
FILING DATE:
FLING DATE:
FLING DATE:
FEGISTALION: NO 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblow, No. 530663ama F.
REGISTRATION NUMBER: 54,618
REFERENCE/PCCKET NUMBER: 583-179-0
TELLEPHONE: (703) 413-220
TELLEPHONE: (703) 413-220
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TELLEPHONE: (703) 413-220
TELLEPHONE: (703) 413-220
TELLEPHONE: (703) A13-220
US-08-468-609A-84
US-08-446-872A-72
US-08-446-872A-75
US-08-46-872A-78
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PCT-US-01185-78
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                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
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nucleic acid
   CDS
1..639
     STRANDEDNESS
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US-08-104-445-2
     Sequence 2, Appli
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*

(cgn2_6/ptodata/2/ina/5B_COMB.seq:*

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(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

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                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-570-856B-2

US-08-963-500-2

US-08-963-500-2

US-08-469-318-177

US-08-469-318-177

US-08-468-609A-177

US-08-446-872A-177

US-08-446-872A-177

US-08-446-872A-178

US-08-446-872A-178

US-08-468-609A-178

US-08-469-118-53

US-08-469-318-75

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Maximum Match 100%
Listing first 45 summaries
                                                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext
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566 AIGITITICGGCAACCGCCTCTGCAGCTGGCACAGATTACTGGCAAAATTGGACGG 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 TIGITITICGGCAACCGCCTCTGCAGCTAGCACACACTACTGGCAAAATTGGACTGATGG 510
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                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Benezien, Joerg M
APPLICANT: Daniyat, Bassil I
TILE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REPERENCE: A-67478-1/RFY/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT PILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PALCHIN Version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.9%; Score 79; DB 4; Length 1349; 79.0%; Pred. No. 1.6e-16; ive 0; Mismatches 25; Indels
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DETERMINESTER:
CORPANIOS SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,964
FILING DATE: 20-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08575964
Patent No. 5736384
| Patent No. 5736384
| CENERAL INFORMATION:
| APPLICANT: Fukunaga, No. 5736384uyuki
| APPLICANT: Fukunaga, No. 5736384uyuki
| APPLICANT: Kono, Satoko
| APPLICANT: Kita, Yukio
| APPLICANT: Kita, Yukio
| APPLICANT: Kita, Yukio
| APPLICANT: Izumi, Yoshiya
| TITE OF INVENTION: THERMOSTABLE XYLANASE
| NUMBER OF SEQUENCES: 3
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Fish & Richardson P.C.
| STREET: 4225 Executive Square, Suite 1400
| CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESSEES | CONTRICTION OF ADDRESS
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                                                                                                             121 AGGACTCCGTTAGGTCCAGCCA 142
                                                                                                                                                                            626 GGCGGGACAGTAAACGCAGTCA 647
                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09570856B Patent No. 6682923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bacillus circulans US-09-570-856B-2
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Matches 94; Conserv
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APPLICANT: GOTTSCHALK, MICHAEL
APPLICANT: GOTTSCHALK, MICHAEL
APPLICANT: SPROBSSIER, ERWIN
TITLE OF INVENTION: BACTERIAL XYLANASE, METHOD FOR ITS
TITLE OF INVENTION: BACTERIAL XYLANASE, PLASMID CONTAINING THE DNA FRAGMENT;
TITLE OF INVENTION: BAKING AGENTS CONTAINING A XYLANASE, AND METHOD FO
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
STREET: Alington
STREET: U.S.A.
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                                                                                                                                                                                                                                                                                  61 ATGTTTTCTGCAACCGCCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGGA 120
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                                                                                                                                                                                                         1 ATGITTAAGITTAAAAAAAATTCITAGIGGGATTAACGGCAGCITTCAIGAGIATCAGC 60
                                                                                                                                              1 ATGITTAAGTITTAAAAAGAAATTCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC
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49.6%; Score 89.2; DB 1; Length 1413;
Best Local Similarity 76.8%; Pred. No. 6.7e-20;
Matches 109; Conservative 0; Mismatches 33; Indels 0;
   Length 642;
                                                                            33; Indels
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Score 89.2; DB 1;
Pred. No. 4.8e-20;
0; Mismatches 33
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FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5306633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 583-179-
TELEPHONE: (703) 413-3000
FELEFAX: (703) 413-220
FELEFAX: (703) 413-220
FELEFAX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FENGTH: 1413 base pairs
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/104,445
                                                                                                                                                                                                                                                                                                                                                                                                                      121 AGGACTCCGTTAGGTCCAGCCA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GGCGGGACAGTÁAACGCÁGTCÁ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application 08/104445 Patent No. 5306633
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MOLECULE TYPE: DNA (genomic)
49.6%;
ilarity 76.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid_
STRANDEDNESS: unknown
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: GOTTSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: un
                                                                     Matches 109;
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US-08-104-445-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.2%; Score 50.8; DB 2; Length 1: Best Local Similarity 74.4%; Pred. No. 3.2e-07; Matches 64; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,318 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

28.1%; Score 50.6; DB 3;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4;
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Fatent No. 6022535
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant IL-
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE SESTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/446,872
FILING DATE:
       TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORIGINALS: STRAIN: 2113
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MOLECULE TYPE: DNA (genomic)

US-08-469-318-177
                                                                                                                                                                                                                                                                        FEATURE:

NAME/KEY: P CDS

LOCATION: 379...1029

LDENTIFICATION METHOD: D:

OTHER INFORMATION:

US-08-963-500-2
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SEQUENCE CHARACTERISTICS:
LENGTH 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -08-469-318-177
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28.2%; Score 50.8; DB 1;
Best Local Similarity 74.4%; Pred. No. 3.2e-07;
Matches 64; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KESULT 5
US-08-963-500-2
Sequence 2, Application US/08963500
Patent No. 5916795
GENERAL INFORMATION:
APPLICANT: Fukunaga No. 5916795uyuki
APPLICANT: Kono, Satoko
APPLICANT: Kono, Satoko
APPLICANT: Izumi, Yuji
APPLICANT: Izumi, Yoshiya
TITLE OF INVENTION: THERMOSTABLE XYLANASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: Ma
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REGISTATION NUMBER: 38,347
REPERENCE/DOCKET NUMBER: 07898/002001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               by experiment
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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
APPLICATION NUMBER: US/08/963,500
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATGITITCIGCAACCGCCTCTGCAGC 86
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/575,964
ALTING DATE: 20-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REFERENCE/DOCKET NUMBER: 0789
TELECOMMUNICATION INFORMATION:
TELEFRAX: 619/678-509
TELEFAX: 619/678-509
TELEFAX: 610/678-509
TELEFAX: 100154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 base pairs :
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Bacillus sp.
STRAIN: 2113
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: P CDS
LOCATION: 379...1029
IDENTIFICATION WETHOD: b
OTHER INFORMATION:
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619/678-5099
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APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Reston, Alan M.
APPLICANT: Ricin, Barbara K.
APPLICANT: Ricin, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Peter O.
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Pusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Corporate P.:
ADDRESSEE: Corporate P.:
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28.1%; Score 50.6; DB 3; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels 0
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MEDIUM TYPE: Flopped disk

MEDIUM TYPE: Flopped disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOUTHARE: Patentin Release #1.0, Version #1.25

SOUTHARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 08/468,609A

RILING DATE: 14-FEB-1994

ATTORNEY AGENT INFORMATION:

NAME: Bennett, Dennis A.

REGISTRATION NUMBER: 34,547

REFERENCE/DOCKET NUMBER: C-2790/3

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Dennis A. Bennett, G.D. Searle & Co.,
E: Corporate Patent Dept.
P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 178, Application US/08468609A Patent No. 6030812
ATTORNEY/AGENT INFORMATION:
NAME: BENDECK, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-275
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (314)737-6976
TELEPHONE: (314)737-6972
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (314)737-6986
TELEFAX: (314)737-6986
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   LENGTH: 546 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TOPOLLOGY: linear
MOLECULE TYPE: DNA (genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 546 base pairs
TYPE: nucleic acid
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-08-468-609A-178
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APPLICANT: Bauer, S. C.
APPLICANT: Bauer, S. C.
APPLICANT: Bauer, S. C.
APPLICANT: Batord-Goldberg, Sarah R.
APPLICANT: Baston, Maire H.
APPLICANT: Caparon, Maire H.
APPLICANT: Caparon, Maire H.
APPLICANT: Klein, Barbara K.
APPLICANT: Alein, Barbara K.
APPLICANT: Thomas, John P.
APPLICANT: Thomas, John P.
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTY: USA
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28.1%; Score 50.6; DB 3; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels (
                                                                            TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA:

RELING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 177, Application US/08468609A Patent No. 6030812 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PARIOR APPLICATION NUMBER: 08/446,872
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inportation for SEQ ID NO: 178:
SEQUENCS CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPROGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-469-318-178
          Patent No. 6022535
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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US-08-468-609A-177
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7 ACACCATTAGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 63

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RESULT 11
US-08-446-872A-178
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28.1%; Score 50.6; DB 4; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels
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APPLICANT: Brafor.
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APPLICANT: Gaparon, Ma...
APPLICANT: Caparon, Ma...
APPLICANT: APPLICANT: Klein, Barbara K.
APPLICANT: MCKearn, John P.
APPLICANT: MCKearn, John P.
APPLICANT: Paik, Kunnan
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-UNN-1995
CLASSIFICATION 424
PRIOR APPLICATION 1424
PRIOR APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.

REGISTRATION NUMBER: 34,547
REPERENCE/DOCKET UNBER: C-2790/1
TELEPHONE: (314,737-6986
                                                                                                                                                                                                 Query Match
28.1%; Score 50.6; DB 3;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 177, Application US/08446872A Patent No. 6361977
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MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-468-609A-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic)
US-08-446-872A-177
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TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-446-872A-177
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28.1%; Score 50.6; DB 4; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:

COUNTRY:

COUNTRY:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM:

CONTRAING SYSTEM:

CONTRAING SYSTEM:

CONTRAING SYSTEM:

CONTRAING SYSTEM:

APPLICATION NUMBER: US/08/446,872A

FILING DATE: 06-UN-1995

CLASSIFICATION: 424

PRIOR APPLICATION 1424

PRIOR APPLICATION HUMBER: US/08/192,325

FILING DATE: 14-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Beneatt, Dennis A.

REGISTRATION NUMBER: 34,547

RECISTRATION NUMBER: 34,547

RETERENCE/DOCKET NUMBER: 34,547

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: 34,547

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TELECOMMUNICATION NUMBER: 34,547

TELECOMMUNICATION NUMBER: 34,547
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis TITLE OF INVENTION: TELBION Protein NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Dennis A. Bennett, G.D. Searle & Co., SIREET: COrporate Patent Dept. STREET: P. O. Box 5110
                                                                                                                              Bauer, S. C.
Brafcord-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Palk, Kumman
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Sequence 178, Application US/08446872A; Patent No. 6361977; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: (314)737-69/2
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 ACTCCGTTAGGTCCAGCCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                  Thomas, John W.
                                                                                                    Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chicago
: Illinois
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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APPLICANT:
APPLICANT:
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124 ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180

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Paik, Kumnan

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28.1%; Score 50.6; DB 4; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRIT APPLICATION DATA:

APPLICATION NUMBER: US/08/762,227A

FILING DATE: 09-Dec-1996

CLASSIFICATION: VUNKNOWN>

PRIOR APPLICATION OWNER: US 08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/192,325

FILING DATE: 06-JUN-1995

ATTORNY/AGENT INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
STREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                          Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
Fusion Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AppLICANT: Abrams, Mark A.
Bauer, S. C.
Brafford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Braford-Goldberg, Sarah R. Caparon, Maire H. Easton, Alan M. Klein, Barbara K. McKearn, Oóhn P. Olins, Peter O. Paik, Kuman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-2790/5
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 177:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REPERENCE/DOCKET NUMBER: C-275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 178, Application US/08762227A Patent No. 6436387 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-762-227A-177
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124 ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) APPLICATION NUMBER: PCT/US95/01185
FILING DATE: 0.2-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.1%; Score 50.6; DB 4; Length 546; 93.0%; Pred. No. 2.7e-07; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPER: FLOPRY disk
MEDIUM TYPER: FLOPRY disk
MEDIUM TYPER: FLOPRY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: AUNROWN:
PRIOR APPLICATION NUMBER: US 08/192,325
APPLICATION NUMBER: US 08/192,325
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REPERENCE/DOCKET WUMBER: C-2790/5
                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Dennis A. Bennett, G.D. Searle & Co.
Corporate Patent Dept.
STREET: P. O. Box 5110
Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
Pusion Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 178: US-08-762-227A-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 177, Application PC/TUS9501185
; GENERAL INFORMATION:
; APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192325
FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6681
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 546 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.15
Best Local Similarity 93.05
Matches 53; Conservative
                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: USA
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PCT-US95-01185-177
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124 ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
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28.1%; Score 50.6; DB 5; Length 546;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4; Indels
                                                                                                                                 Length 546;
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                                                                                                                                Query Match

28.1%; Score 50.6; DB 5;
Best Local Similarity 93.0%; Pred. No. 2.7e-07;
Matches 53; Conservative 0; Mismatches 4;
                           LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-01185-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) PCT-US95-01185-178
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
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Search completed: October 9, 2004, 04:24:24 Job time: 28.6529 secs

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October 8, 2004, 21:19:03 ; Search time 136.728 Seconds (without alignments) 5592.665 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                       OM nucleic - nucleic search, using sw model
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180
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Perfect score:
Sequence:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

Searched:

6747726

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N. Geneseq. 29Jan04:*

1. geneseqn1980s:*
2: geneseqn2000s:*
4: geneseqn2001s:*
5: geneseqn2001bs:*
6: geneseqn2001bs:*
6: geneseqn2001bs:*
8: geneseqn2003bs:*
9: geneseqn2003bs:* geneseqn2004s:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	£	10	AAD19775	AAQ56052	AAQ66480	AAA47153	AAD19774	AAA47157	AAA47155	AAA47156	AAA47154	AAS13814	ADC27538	AAC88889	AAL48894	AAI71848	AAQ97205	AAQ97206	AAA03772	AAA03773	ABX00088	ABX00087	AAN70029	AAQ97167	AAA03721
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	9100	20016	180	σ.	89.2	7.	98	9.64	9.61	o	79	79	79	79	79	52	50.6	50.6	9.05	50.6	50.6	50.6	50.6	50.6	9.05
-	Result		п	7	m	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

(KOAD) KOREA ADV INST SCI & TECHNOLOGY.

WPI; 2001-616523/71. P-PSDB; AAE12157. Lee S, Jeong K;

906 6 ABX00010 921 2 AAQ97186 921 2 AAQ97186 921 2 AAQ97182 921 3 AAA03742 921 3 AAA03740 921 3 AAA03740 921 6 ABX00032 921 6 ABX00032 921 6 ABX00032 921 6 ABX00032 921 6 ABX00032 926 2 AAQ97184 966 2 AAQ97184 966 2 AAQ97187 966 2 AAQ97187 966 3 AAA03746	Abx00010 Human int Aqg7198 pMON13066 Aqg7189 pMON13013 Aqg7192 pMON131013 Aqg7192 pMON13151 Aqa03746 Human int Aqa03754 Human int Aqa03749 Human int Abx00029 Human int Abx00029 Human int Abx00029 Human int Abx00041 Human int Abx00041 Human int Abx00041 Human int Abx00041 Human int Abx00041 Human int Abx00041 Human int Abx00041 Human int Abx00041 Human int Abx00041 Human int Aqg71191 pMON13045 Aqg97181 pMON13045 Aqg97187 PMON13058	m 01 H 10 W
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the invention relates to an Escherichia coli producing and secreting human granulocyte colony stimulating factor (hd-CSF), more specifically, to a recombinant plasmid constructed to express secretory hd-CSF in E. coli, an E. coli transformed with that plasmid to secrete hd-CSF, and a prodess for preparing hd-CSF using the transformed hd-CSF. The crecombinant plasmid vector comprises of a kananycin resistence gene, a promoter, an endoxylanase signal sequence, a mucleotide sequence coding for an oligopeptide consisting of 13 amino acids including 6 consecutive histidine residues and a hd-CSF. B.coli transformed with recombinant plasmid vector is useful for preparing hd-CSF. The method comprises culturing the microorganism to obtain a hd-CSF fusion protein and tracture protein with a protease preferably Factor Xa, to obtain a hd-CSF, where the fusion protein is obtained from the culture by employing Ni-column. The present sequence is a DNA encoding human hd-CSF NI-terminal region inserted into plasmid pTHSCSFMII
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Recombinant plasmid vector comprising an endoxylanase signal sequence, human granulocyte colony stimulating factor gene and other components, when transformed into microorganism useful for preparing the colony stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGITITAAGITITAAAAGAAATICITAGIGGGATITAACGGCAGCITICAIGAGIAICAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 180; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-50;
Matches 180; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 180 BP; 44 A; 50 C; 40 G; 46 T; 0 U; 0 Other;
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                                                                                                     Fig 12; 50pp; English
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P-PSDB; AAR47200.
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10-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-1994
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61 AIGITITCIGCAACCGCCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGGA 120
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New xylanase obtd. from Bacillus subtilis - useful in baking agents for increased vol. of baking prods.
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                                                                                                                                                                                  1 ATGITTAAGTITAAAAAGAAATTCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC
                                                                                                                                                                                                        1 ATGITIAAGITIAAAAAAAAATICTIAGIGGATIAAAGGGGAGCITICAIGAGIAICAGG
                                                              The modified xylanase is used as a baking agent, preferably for yeast pastry and white bread. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                           Gaps
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                                                                                                                              Query Match

49.6%; Score 89.2; DB 2; Length 642;
Best Local Similarity 76.8%; Pred. No. 1.2e-19;
Matches 109; Conservative 0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U; 0 Other;
                                                                                                      Sequence 642 BP; 191 A; 122 C; 166 G; 163 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1413 BP; 408 A; 280 C; 317 G; 408 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Modified xylanase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence comprising xylanase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.6%; Score 89.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schuster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
506. 1209
/*tag= a
                                                                                                                                                                                                                                                                                           121 AGGACTCCGTTAGGTCCAGCCA 142
                                                                                                                                                                                                                                                                                                                   GGCGGGACAGTAAACGCAGTCA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 9; 11pp; German
                                                                                                                                                                                                                                                                                                                                                                                      ВЭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New xylanase obtd. from Bacillu
increased vol. of baking prods.
                                            Claim 4; Page 10; 11pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sproessler B,
                                                                                                                                                                                                                                                                                                                                                                                    AAQ66480 standard; DNA; 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92DE-04226528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92DE-04226528
                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bread; pastry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROHG ) ROEHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gottschalk M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE4226528-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
10-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                AAQ66480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                             RESULT 3
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Length 642;

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Query Match
Best Local Similarity
Matches 108; Conserv
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                                                                                                                                                                                                                                                            RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also describes an endo-bece. It also becent in the framework in the specification also describes a mutant xylanase in the wheat flour. The specification also describes a mutant xylanase from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a product. Wild type xylanase or mutant xylanase is useful for preparing a dought hat is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for spreparing a long preparation of xylanase and the inhibitor is useful for calibrating and/or determining the quantity of inhibitor in a wheat flour sample
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                                                                           565
                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encodes an endo-beta-1,4-xylanase. The specification
                                                                                                                                      56 ATGTTTTCGGCAACCGCTCTGCAGCTGGCACAGATTACTGGCAAAATTGGACTGACGGG 625
                                               9
                                                                                                                                                                                                                                                                                                                                                                                               Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.
                                                                                                         ATGTTTTCTGCAACCGCCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGGA
                                               ATGITITAAGITITAAAAAAAATITCITAGIGGGATITAACGGCAGCITITCAIGAGIAICAGC
                                                                           506 ArgritaAgrirraAAAAAAArrcriAGriGGATTAACGGCAGCTTTCATGAGTATCAGC
                   Gaps
                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 642 BP; 192 A; 122 C; 164 G; 164 T; 0 U; 0 Other;
                 Indels
                                                                                                                                                                                                                                                                                                                                                                DNA encoding a bacterial endo-beta-1,4-xylanase protein.
   Pred. No. 1.7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 107; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "xylanase"
                                                                                                                                                                  121 AGGACTCCGTTAGGTCCAGCCA 142
                                                                                                                                                                                                 626 GGGGGACAGTÁAACGCÁGTCA 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                          AAA47153 standard; DNA; 642 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98GB-00028599.
99GB-00007805.
99GB-00008645.
                                                                                                                                                                                                                                                                                                                                                                                                                dough; dough preparation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-IB002071
   76.8%;
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sibbesen O, Sorensen JF;
                   109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
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Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DANI-) DANISCO AS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAY93751.
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15-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1998;
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                                                                                                                                                                                                                                                                                                       AAA47153;
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                                                                                                                   61 ATGITITCIGCAACCGCCICIGCAGCIGGCCCGCACCAICACCAICACCAIAICGAGGGA 120
                                                                                                                                               61 ATGITITICGGCAACCGCCTCTGCAGCTGGCACAGATTACTGGCAAAATTGGACTGACGGG 120
                                                            9
                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an Bscherichia coli producing and secreting human granulocyte colony stimulating factor (hG-CSE), more specifically, how a recombinant plasmid constructed to express secretory hG-CSF in E-coli, an E-coli transformed with that plasmid to secrete hG-CSF, and a process for preparing hG-CSF using the transformed hG-CSF. The recombinant plasmid vector comprises of a kanamycin resistance gene, a promoter, an endoxylanase signal sequence, a nucleotide sequence coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant plasmid vector comprising an endoxylanase signal sequence, human granulocyte colony stimulating factor gene and other components, when transformed into microorganism useful for preparing the colony stimulating factor.
                                                            1 ATGITTAAGTITAAAAAGAAATTCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC
                                                                                     ArgritaAgritaAAAAAAAATrcritAGritGGATTAACGGCAGCTTTCATGAGTATCAGC
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Human, granulocyte colony stimulating factor; hG-CSF; protease; Factor Xa; kanamycin resistance; endoxylanase signal peptide; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human mature hG-CSF protein fragment"
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0
                                                                                                                                                                                                                                                                                                                                                                       into plasmid pTrcSCSFmII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hG-CSF protein fragment"
not include stop codon"
                               34; Indels
Score 87.6; DB 3;
Pred. No. 4.2e-19;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
                                                                                                                                                                              142
                                                                                                                                                                                                          121 GGCGGGACAGTAAACGCAGTCA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        DNA 5' end inserted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Human
/note= "CDS does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Fig 9; 50pp; English.
                                                                                                                                                                              121 AGGACTCCGTTAGGTCCAGCCA
                                                                                                                                                                                                                                                                                  BP
   48.7%;
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                                                                                                                                                                                                                                                                                  AAD19774 standard; DNA; 135
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/product=
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P-PSDB; AAE12156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jeong K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200173081-A1
                                                                                                                                                                                                                                                                                                                                                                          Human hG-CSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                          18-DEC-2001
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for an oligopeptide consisting of 13 amino acids including 6 consecutive histidine residues and a hG-CSF. B.coli transformed with recombinant plasmid vector is useful for preparing hG-CSF. The method comprises culturing the microorganism to obtain a hG-CSF fusion protein and treating the fusion protein with a protease preferably Factor Xa, to obtain a hG-CSF, where the fusion protein is obtained from the culture by employing Ni-column. The present sequence is a DNA encoding human hG-CSF
                                                                                                                                                                                                                                                                                         ATGITITCTGCAACCGCCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGGA 120
                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product; dough; dough preparation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a mutant endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                              1 ATGITTAAGTTTAAAAAGAAATTCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC
                                                                                                                                                                                                                                                          ATGITIAAGITITAAAAAAAATITCITAGIGGGATIAACGGCAGCITITCAIGAGIAICAGC
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                              ---ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCAGAGCTTCCTGCTCAAGTGC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               using xylanase inhibitor useful
                                                                                                                                                                                                                                                                                                                                                    121 AGGACTCCGTTAGGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGC
                                                                                                                                                                                                39;
                                                                                                                                                                 Score 86; DB 4; Length 135;
Pred. No. 7.8e-19;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a bacterial endo-beta-1,4-xylanase mutant XM3
                                                                                                                                       Sequence 135 BP; 32 A; 36 C; 28 G; 39 T; 0 U; 0 Other;
                                                                                                          N-terminal region inserted into plasmid pTrcSCSFMII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutant xylanase protein identified using xylane preparing non-sticky dough for bakery products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "xylanase mutant"
                                                                                                                                                                                                 0; Mismatches
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99GB-00007805.
99GB-00008645.
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                                                                                                                                                                   47.8%;
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P-PSDB; AAY93755.
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                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
Bacillus subtilis.
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06-APR-1999;
15-APR-1999;
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                                                                                                                                                                                                 Matches 135;
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61 ATGITITCIBCAACCGCCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGGA 120
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is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for preparing a non-sticky dough. A combination of xylanase and the inhibitor is useful for callibrating and/or determining the quantity of inhibitor in a wheat flour sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
dough; dough preparation; ss.
                                                                                                                                                                                                                                                                                                        Argittaagittaaaaagaartictiagitggattarcggcagcittaargagtartagc
                                                                                                                                                                                                                                                                             1 ATGITTAAGITTAAAAAGAAATTCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant xylanase protein identified using xylanase inhibitor useful
preparing non-sticky dough for bakery products.
                                                                                                                                                                                                           44.2%; Score 79.6; DB 3; Length 642; ilarity 72.5%; Pred. No. 2.1e-16; Conservative 0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding a bacterial endo-beta-1,4-xylanase mutant XM1
                                                                                                                                                                              Sequence 642 BP; 192 A; 110 C; 162 G; 178 T; 0 U; 0 Other;
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/product= "xylanase mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGTACCGTAACGCTGTCA 142
                                                                                                                                                                                                                                                                                                                                                                                                        121 AGGACTCCGTTAGGTCCAGCCA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
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99GB-00007805.
99GB-00008645.
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P-PSDB; AAY93753.
                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DANI-) DANISCO AS.
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06-APR-1999;
15-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sibbesen O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA47155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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XX SQ Sequence 546 BP; 95 A; 189 C; 157 G; 105 T; 0 U; 0 Other;

Query Match 28.1%; Score 50.6; DB 2; Length 546; Best Local Similarity 93.0%; Pred. No. 1.2e-06; Matches 53; Conservative 0; Mismatches 4; Indels 0; Gaps

0;

ò Dp Search completed: October 9, 2004, 02:07:18 Job time: 138.728 secs

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alkalophilicity, or thermostability relative to naturally occurring B. circulans xylansse, and has at least 5 amino acid substitutions. A bleaching agent comprising a modified xylansse is useful for bleaching pulp, in the bioconversion of lignocellulosic materials to fuels, for clarifying juice and wine, extracting coffee, plant oils and starch, producing food thickeners, altering texture in bakery products, e.g. improving the quality of dough, helping bread to rise and processing of wheat and corn for starch production, use as animal food additives to aid in the digestibility of feedstuffs and in the washing of super precision devices and semiconductors. The present sequence is a coding sequence of a xylanase protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                        451
                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for producing recombinant human granulocyte colony stimulating factor (FnG-CSF). The method includes the following steps: (a) reverse transcription-polymerase chain reaction of the human granulocyte colony stimulating factor gene; (b) transforming Escherichia coli, (c) renaturation of protein by hollow fibre ultrafiltration dialysis; (d) passing the renatured protein through ion exchange chromatography, hydrophobic chromatography and molecular sieve
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ATGITITUTGCAACCGCCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     granulocyte colony stimulating factor; rhG-CSF; recombinant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  392 ATGITTAAAAAAAAATTITCITAGITAGATTATCGGCAGCITTAATGAGTATTAGC
                                                                                                                                                                                                                                                                                                                                                                   1 ATGITIAAGITIAAAAAGAAATICITAGIGGGAITAACGGCAGCITICAIGAGIAICAGC
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 TIGITITICGGCAACCGCCTCTGCAGCTAGCACAACTACTGGCAAAATTGGACTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Production of recombined human granulocyte colony stimulation factor.
                                                                                                                                                                                                                                                                                                                                 ..
protein has been modified to exhibit enhanced thermophilicity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant human granulocyte colony stimulating factor cDNA.
                                                                                                                                                                                                                                                                                    ch 43.9%; Score 79; DB 6; Length 1349; I Similarity 79.0%; Pred. No. 4.5e-16; 94; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                    Sequence 1349 BP; 396 A; 232 C; 312 G; 409 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 8 (disclosure); 15pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JIUY-) JIUYUAN GENE ENG CO LTD HANGZHOU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94. .621
/*tag= a
/product= "rhG-CSF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI71848 standard; cDNA; 644 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96CN-00106418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96CN-00106418,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-590346/67.
                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-590346/
P-PSDB; AAMS1536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kong T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI71848;
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Su Y,
                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human cartebusin-3 (h1L-3), R2 is a second colony stimulating factor (CSF) including cytokine, lymphokine, interleukin, haematopoietic growth factor or IL-3 variant and L is a linker. Generic sequences are described in ARN9228-R79335 and specifically claimed examples are shown in AAR7928-R79342. The fusion protein is made by recombinant DNA techniques. Specifically claimed examples of DNA recombinant DNA techniques. Specifically claimed examples of DNA recombinant DNA techniques. Specifically claimed examples of DNA AR79222-Q97227. The fusion protein is used to increase haematopoietic claimed examples of DNA argonator or antibodies useful in immunoassays and immunotherapy. Antagonists are used to block the growth of certain cancer cells and in treatment of asthma. The fusion protein can also be used to stimulate bone marrow and blood cell activation and growth in vitro before infusion; and to treat diseases characterised by decreased levels of myeloid, erythroid, lymphoid and/or megakaryocyte cells of the haematopoietic system. The protein has the usual activity of both its component proteins, but may have increased synergistic activity and reduced undesired side effects
                                                                                                                                                 ö
                                                                                                                                                                                    121 AGGACTCCGTTAGGTCCAGCCAGCTCCCTGCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
                                                                                                                                                                                                           stimulating factor; cytokine; lymphokine;
linker; ss.
   (e)
rhG-CSF
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Easton AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion proteins comprising a human interleukin-3 variant, a linker a interleukin-3, a variant or a colony stimulating factor - useful to increase haematopoietic cell prodn. in a mammal.
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chromatography which are combined together sequentially, and purifying so to obtain a high yield of high-purity medicinal protein. The present sequence encodes rhG-CSF
                                                                                                               Length 644;
                                                                        U; 0 Other;
                                                                                                             Score 52; DB 5; Length 644
Pred. No. 4.2e-07;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caparon MH,
Thomas JW;
                                                                          Sequence 644 BP; 128 A; 216 C; 172 G; 128 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Braford-Goldberg SR,
Olins PO, Paik K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 15; Page 183-184; 447pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin; hIL-3; CSF; colony
mutant; mutein; fusion protein;
                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US001185.
                                                                                                             28.9%;
ilarity 91.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                AAQ97205 standard; DNA; 546
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                        pMON13010 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abrams MA,
Mckearn JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-283774/37.
                                                                                                         Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAR79336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09521254-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                     25-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bauer CS,
Klein BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                      94
                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                               AAQ97205
     88888
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This invention relates to a novel variant xylanase protein or its fragment having xylanase activity. The variants have one or more amino caid modifications so that the protein or fragment has an altered consistency to a xylanase inhibitor and has an altered thermosensitivity as ensitivity to a xylanase inhibitor and has an altered thermosensitivity as compared with a parent xylanase enzyme. The variant xylanases of the invention are useful for degrading or modifying a plant cell wall, and for processing cereals, starch production, in processing wood, and enhancing the blacking of wood pulp. They may also be useful for a variety of applications such as animal feed, flour separation (wetmilling) and paper of lour dough. The enzymes of the invention may alter or reduce the resonance of the invention may alter or reduce the viscosity derived from the presence of hemicellulose or arabinoxylan in a colution or system comprising plant cell wall material, and for modifying codard/or feed supplement comprising xylan. Use of the variant contraint processes improves the properties of flour based doughs and products made from the doughs. The baked products have highly desirable characteristics with respect to blood volume, crumb structure and appearance and additionally have an extended shelf-life. The enzymes of the invention have reduced thermosensitivity and inhibitor and products and additionally have an extended shelf-life xylanase required for animal feed, starch production in the amount of xylanase required the construction and baking. The present sequence is the column and paking. The present sequence is
                                              Novel variant xylanase polypeptide having altered sensitivity to a xylanase inhibitor and altered thermosensitivity as compared with a parent xylanase enzyme, useful in baking, processing cereals, starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which was used to create the variant xylanases of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 79; DB 9; Length 645;
Pred. No. 3.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 645 BP; 192 A; 111 C; 163 G; 179 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                        Example 2; Page 38; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.9%;
P-PSDB; ADC27541, ADC27530.
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                                                                                                                            61 ATGITITCIGCAACCGCTCTGCAGCTGGCCGCACCATCACCATCACCATATCGAGGG 119
                                                                                                                                                          64 TIGITITICGGCAACCGCCTCTGCAGCTAGCACACACTACTGGCAAAATTGGACTGATGG 122
                                          1 ATGITTAAGITTTAAAAGAAATTCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC
                                                                               4 Argitiaagititaaaagaatiticitagitggattaticggcagcittaatgagtaftagc
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Bacillus circulans; xylanase; xylanase activity; XA; bleaching agent; ds
                                                     Bacillus circulans xylanase DNA sequence.
             멾
            AAC88889 standard; DNA; 1349
                                       (first entry)
                                                                                Bacillus circulans
                                        05-MAR-2001
                          AAC88889
      AAC88889
RESULT
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10-NOV-2000; 2000US-00710050

(XENC-) XENCOR INC

WPI; 2002-608200/65

Bentzien J,

09-NOV-2001; 2001WO-US048018

16-MAY-2002

The present invention relates to a non-naturally occurring xylanase activity (XA) protein comprising an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase, where the Novel xylanase activity protein, useful in bleaching process of pulp and in food and animal feed industry, has enhanced thermostability and Disclosure; Fig 1C; 121pp; English. alkalophilicity.

99US-0133714P

12-MAY-1999;

(XENC-) XENCOR INC

12-MAY-2000; 2000WO-US013172

WO200068396-A2.

16-NOV-2000

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                                                                                                                                                                                                                                                                                                                                                                           451
                                                                                                                                              The present sequence is given in a specification relating to non naturally occurring xylanase activity (XA) proteins. The XA proteins comprise an amino acid sequence less than 97% identical to a naturally occurring Bacillus circulans xylanase. They are modified to exhibit enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring B. circulans xylanase. They may be used as the active compound in a bleaching agent which is used for bleaching pulp
                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                        119
                                                              Non naturally occurring XA protein with enhanced thermophilicity, alkalophilicity or thermostability relative to the naturally occurring Bacillus circulans xylanase is used in an agent for bleaching pulp.
                                                                                                                                                                                                                                                                                                                                              1 ATGITIAAGITITAAAAAAAAATICTTAGIGGGATTAACGGCAGCTITCAIGAGIAICAGC
                                                                                                                                                                                                                                                                                                                                                                          392 Argirirakgirirakakakakirichiragiragarirarcagcagcirirakigagirirake
                                                                                                                                                                                                                                                                                                                                                                                                     61 AIGITITCIGCAACGGCCICTGCAGCTGGCCGCCCACCATCACCATCACCATATCGAGGG
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylanase activity, enzyme; thermostable; xylanase; pulp bleaching; liquid clarification; coffee extraction; plant oil extraction; gene; starch extraction; food thickener; animal food additive; mutant; ds.
                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                        Score 79; DB 3; Length 1349;
Pred. No. 4.5e-16;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                              Sequence 1349 BP; 396 A; 232 C; 312 G; 409 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B circulans xylanase coding sequence.
                                                                                                                        Disclosure, Fig 1C; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL48894 standard; DNA; 1349
                                                                                                                                                                                                                                                                                             43.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 79.0
Matches 94; Conservative
                            2000-679800/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus circulans
                          WPI; 2000-679800
P-PSDB; AAB48530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO200238746-A2
Sentzien JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
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(DANI-) DANISCO AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC27538;
                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                       also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Whid type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase is useful for screening high degree resistance xylanase for dough preparation. The xylanase is also useful for preparing a preparation and/or determining the quantity of inhibitor in the set of the constitution of the inhibitor in the set of the constitution of the inhibitor in the xylanase and the inhibitor in the xylanase and the inhibitor in the xylanase and the inhibitor in the xylanase and the similar and/or determining the quantity of inhibitor in
                                              The specification
                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                     119
                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                     61 ATGITITICIGCAACCGCCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel variant xylanase polypeptide or its fragment useful for degrading or modifying plant cell wall, comprises amino acid modifications such that the polypeptide has altered sensitivity to xylanase inhibitor.
                                                                                                                                                                                                                                                                                                                                         1 ATGITTAAGTITTAAAAAGAAATTCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                61 TIGITITICGCAACCGCCTCTGCAGCTAGCACAAACTGGCAAAATTGGACTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant cell wall; baking; cereal; starch production; wood; bleaching; hemicellulose; arabinoxylan; foodstuff; ds.
                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                          Score 79; DB 3; Length 642;
Pred, No. 3.4e-16;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                Sequence 642 BP; 191 A; 110 C; 163 G; 178 T; 0 U; 0 Other;
                                          The present sequence encodes an endo-beta-1,4-xylanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding Bacillus subtilis xylanase
              Disclosure; Page 108; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 98. .645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "xylanase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 43; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2001; 2001WO-1B000426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2000; 2000GB-00005585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUN-2000; 2000GB-00015751
                                                                                                                                                                                                                                                                            ch 43.9%;
1 Similarity 79.0%;
94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS13814 standard; DNA; 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sibbesen O, Sorensen
                                                                                                                                                                                                                a wheat flour sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-596834/67.
P-PSDB; AAU07391.
                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DANI-) DANISCO AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xylanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wood pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS13814;
                                                                                                                                                                                                                                                                             Query Match
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The invention relates to a variant xylanase polypeptide (I) or its fragment having xylanase activity, comprising one or more amino acid modifications such that (I) or its fragment has an altered sensitivity to a xylanase inhibitor as compared with the parent xylanase enzyme. (I) or its coding sequence (II) is useful for degrading or modifying plant cell wall or for processing a plant material by contacting the plant cell wall or plant material with (I) or (II): (I) is useful for modifying plant materials, and in baking, processing cereals, starch production, processing wood and enhancing the bleaching of wood pulp. (I) is useful or altering the viscosity derived from the presence of hemicellulose or arabinoxylan in a solution or system comprising plant cell wall material.

(I) is useful for preparing a foodstuff such as bread, pretzels, tortillas, cakes, cookies, biscuits or crackers. The present sequence represents the coding sequence of Bacillus subtilis xylanase as described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATGTTTTCTGCAACCGCCTCTGCAGCTGGCCCGCACCATCACCATCACCATATCGAGGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Argitiaagititaaaaagaarrictiagiricgarracgccaccritaargagrarragc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGTTTAAGTTTAAAAGAAATTCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xylanase; xylanase inhibitor; thermosensitivity; plant cell wall; plant material; baking; processing cereal; starch production; processing wood; wood pulp bleaching; animal feed; flour separation; wetmilling; paper and pulp production; flour dough; hemicellulose; arrabinoxylan; food supplement; xylan; baking process; bread volume; crumb structure; crumb appearance; shelf-life; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product = "Bacillus subtilis xylanase enzyme"
                                                                                                                                                                                                                                                                                                                                                                   Sequence 645 BP; 192 A; 111 C; 163 G; 179 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88. _642
/*tag= c
/label= Mature_Bacillus_subtilis_xylanase
                                                                                                                                                                                                                                                                                                                                                                                                         Score 79; DB 5; Length 645
Pred. No. 3.4e-16;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis xylanase enzyme cDNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC27538 standard; cDNA; 645 BP.
                                                                                                                                                                                                                                                                                                                                                                                                           ch 43.9%;
1 Similarity 79.0%;
94; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-AUG-2002; 2002WO-IB003797.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4. .645
/*tag=
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Claim 3; Page 110; 112pp; English.
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                                                                                                                                                                                                                                                                                        Trefririceschaccectrerecaschadeachagaeracascharatresacreareas 120
          specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant sylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for preparing a non-sticky dough. A combination of xylanase and the inhibitor is useful for calibrating and/or determining the quantity of inhibitor in a wheat flour sample
                                                                                                                                                                                                                     1 ATGITIAAGITIAAAAAGAAATICITAGIGGGATTAACGGCAGCITICAIGAGIAICAGC 60
                                                                                                                                                                                                                                           Arcittaagtitaaaaagaatticttagitggattarcggcagcittaatgagtagtagc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.
                                                                                                                                                                                                  Gaps
    present sequence encodes a mutant endo-beta-1,4-xylanase. The
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                                                                                                                                                                        Score 79.6; DB 3; Length 642; Pred. No. 2.1e-16; 0; Mismatches 39; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a bacterial endo-beta-1,4-xylanase mutant XM2
                                                                                                                                                     Sequence 642 BP; 187 A; 115 C; 162 G; 178 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "xylanase mutant"
                                                                                                                                                                                                                                                                                                                   121 AGGACTCCGTTAGGTCCAGCCA 142
                                                                                                                                                                                                                                                                                                                                          121 GGCGGTACCGTAAACGCTGTCA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .642
                                                                                                                                                                                                                                                                                                                                                                                                AAA47156 standard; DNA; 642 BP
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99GB-00007805.
99GB-00008645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dough; dough preparation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-IB002071
                                                                                                                                                                           Query Match
Best Local Similarity 72.5%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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P-PSDB; AAY93754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DANI-) DANISCO AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
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06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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The present sequence encodes a mutant endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less suicky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree for preparing a non-sticky dough. A combination of xylanase and the inhibitor is useful for allorable and continuing the quantity of inhibitor in a wheat flour sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endo-beta-1.4-xylanase inhibitor; wheat flour; xylanase; bakery product; dough; dough preparation; ss.
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preparing non-sticky dough for bakery products.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                 44.2%; Score 79.6; DB 3; Length 642; larity 72.5%; Pred. No. 2.1e-16; Conservative 0; Mismatches 39; Indels (
                                                                                                                                                                                                                                                                                                                                                                              Sequence 642 BP; 189 A; 113 C; 161 G; 179 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONA encoding a bacterial endo-beta-1,4-xylanase protein.
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/product= "xylanase"
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99GB-00007805.
99GB-00008645.
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/*tag=
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hes 103; Conserv
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06-APR-1999;
15-APR-1999;
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October 8, 2004, 21:23:54; Search time 937.383 Seconds (without alignments) 8322.904 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SOURCE BACLILUS SP. ORGANISM Bacillus S. Bacteria: Firmicutes: Bacillales: Bacillaceae; Bacillus.

Gaps

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PAT 17-JUL-2003

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Gaps

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QSKRPTGSNAAITFSNHVNAWKSHGMNLGSNWAYQVLATEGYKSSGSSNVTVW"
                                                                                                                                                                                                                                                                                                                      61 ATGITITCIGCAACCGCCICIGCAGCTGGCCCGCACCAICACCAICACCAIAICGAGGGA 120
                                                                                                                                                                                                                                                                                                                                                      61 ATGTTTTCGGCAACCGCCTCTGCAGCTGGCACAGATTACTGGCAAAATTGGACTGACGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis
Bacillus subtilis
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
1 (Joases 1 to 1413)
Gottschalk, M.D., Schuster, B.D. and Sproessler, B.D.
Bacterial Xylanase, method for its production and its application in manufacturing bread
Patent: EP 058517-A 1 09-MAR-1994;
ROEHM GMBH (DE)
                                                                                                                                                                                                                                         1 ATGITTAAGITTAAAAAGAAATTCITAGIGGGATTAACGGCAGCITTCAIGAGTATCAGC
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llarity 76.8%; Pred. No. 4.3e-19;
Conservative 0; Mismatches 33;
                                                                                                                                                        Score 89.2; DB 6;
Pred. No. 3.7e-19;
0; Mismatches 33;
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/organism="Bacillus subtilis"
/mol type="unassigned DNA"
/strain="XH 1321"
/db_xref="taxon:1423"
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Other publication FF 933519 940212
Other publication DE 4226528 940217.
Location/Qualifiers
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llarity 76.8%;
Conservative
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Best Local Similarity
Matches 109; Conserv
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Best Local Similarity
Matches 109; Conserv
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BD234184
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                                                                                                                                                                                                                                                                                                                                           /product="endo-1,4-beta-xylanhydrolase"
|product="endo-1,4-beta-xylanhydrolase"|
|db.cref="d1:40471"|
|translation="MFKFKKRPLVGLTAAFMSISMFSATASAAGTDYWQNWTDGGGTV
|htranslation="MFKFKKRPLVGKGWTGSPRFINYNAGWARDRGNTLTVGWTRA
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QSKRPPGSNAALTFSNRVNAWKSHGMNLGSNNAYQULATEGYKSSGSSNVTVW
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Bacteria, Pirmicutes, Bacillales, Bacillaceae, Bacillus.
1 (Dases 1 to 641)
Gottschalk, M.D., Schuster, E.D. and Sproessler, B.D.
Gottschalk, M.D., Schuster, E.D. and Sproessler, B.D.
andretral Xylanase, method for its production and its application in manufacturing bread
Patent: EP 0585617-A 2 09-MAR-1994;
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Advanced Institute of Science and Technology, 373-1, Kusong-dong Yusong-ku, Taejon 305-701, Korea Location/Qualifiers
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                                                                                                                                                                                                                                                              /note="similar to B. subtilis xylanase, Swiss-Prot
Accession Number P18429"
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0
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larity 77.5%; Pred. No. 1.3e-19;
Conservative 0; Mismatches 32; Indels 0
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/codon start=1
/trans1_table=11
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/mol type="unassigned DNA"
/strain="RH 1321"
                                                                                                                                                                                                                          gene="xynA"
function="xylan hydrolysis"
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Other publication PR 935359 940212
Other publication DE 4225528 940217
Location/Qualifiers
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/mol_type="genomic DNA"
/mb_xref="taxon:1409"
360_ 365
372. 1013
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/protein_id="CAA02246.1"
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Sequence 2 from Patent EP0585617.
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'trans1_table=11
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372. .1013
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Pred. No. 1.3e-18;
0; Mismatches 34; Indels
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DANISCO AS
OS Artificial Sequence
PD 08-OCT-2002
PD 08-OCT-2002
PF 17-DEC-1999 JP 2000591181
PF 23-DEC-1999 GB 982859.2,06-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015-APR-1999 015
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llarity 72.5%; Pred. No. 7.2e-16;
Conservative 0; Mismatches 39;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sibbesen, O. and Soerensen, J.F.
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JP 2002533121-A/3.
    76.18;
Best Local Similarity 76.1<sup>5</sup>
Matches 108, Conservative
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Matches 103; C
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PF 17-DEC-1999 JP 2000591181
PF 77-DEC-1999 GB 9928645.6
15-APR-1999 GB 9908645.6
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PT 0LE STBBESBN,JRNS FRISBAEK SOERENSEN
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SOERENSEN JENS FRISBAEK (DK); DANISCO (DK); SIBBESEN OLE (DK)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGITTAAGTITTAAAAAGAAATTCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC
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/organism='Artificial Sequence'
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                Patent: JP 2002533121-A 1 08-OCT-2002;
DANISCO AS
OS Artificial Sequence
PN JP 2002533121-A/1
PD 08-OCT-2002
PF 17-DEC-1999 JP 2000591181
PR 23-DEC-1999 GB 9828599 2 06-ADD-1
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/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
/mol_tye="unassigned DNA"
/db_xref="reaxon:32630"
/note="wild-type xylanase"
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Sequence 4 from Patent W00039289
AX027170 GI:10188157
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synthetic construct
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1 (bases 1 to 642)
Sibbesen, O. and Soerensen, J.F.
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                                                        GI:33043954
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Best Local Similarity 76.1%;
Matches 108; Conservative
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BD234184.1 GI:330
JP 2002533121-A/1.
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JOURNAL
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TITLE
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PAT 16-SEP-2000
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Proteins
Patent: WO 0039289-A 8 06-JUL-2000;
SOERENSEN JENS FRISBAEK (DK); DANISCO (DK); SIBBESEN OLE (DK)
10.0642
10.0642
10.0642
10.0642
10.065="muranism="synthetic construct"
| Mol_type="unassigned DNA"
| /db_xref="reaxon:32630"
| note="murant xylanase"
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PC C12N9/42,C12P21/02,C12Q1/34,C12N15/00,C12N5/00 CC Description of Artificial Sequence:mutant xylanase FH Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 642;
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44.2%; Score 79.6; DB 6; 1
Best Local Similarity 72.5%; Pred. No. 7.2e-16;
Matches 103; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 72.5%; Pred. No. 7.2e-16; D3; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                        1. .642
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Sequence 10 from Patent W00039289.
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Sequence 8 from Patent W00039289.
AX027174 GI:10188159
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PN JP 2002533121-A/1

PD 09-CCT-2002

PF 17-DFC-1999 GB 9828599.2,06-APR-1999 GB 990/bcc.

PR 23-DEC-1998 GB 9828599.2,06-APR-1999 GB 990/bcc.

15-APR-1999 GB 9828599.2,06-APR-1999 GB 990/bcc.

PR 23-DEC-1998 GB 9828599.2,06-APR-1999 GB 990/bcc.

C12N1/21,012N2/10.2,012N2/26,007K14/415,C12N1/15,C12N1/19,C12N1/20 PC C12N3/42,C12P2/20.2,C12D1/34,C12N1/515,C12N1/19,C12N1/20 PC C12N3/42,C12P2/20.2,C12D1/34,C12N1/215,C12N1/19,C12N1/20 PC C12N3/42,C12P2/20.2,C12N1/20,C12N1/20,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/20.2,C12N1/
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Pred. No. 7.2e-16;
0; Mismatches 39;
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DANISCO AS
DATLIficial Sequence
PN JP 2002533121-A/5
PD 08-OCT-2002
PF 17-DEC-1999 JP 2000591181
PR 23-DEC-1999 GB 9908645.6
PI OLE SIBBEERN/SERNS FRISBARK SOBRENSEN
PC C12N15/09/A21D2/26,COTK14/415,C12N1/
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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DANISCO AS
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                                                                                                               synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 642)
Sibbesen,O. and Soerensen,J.F.
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1 (bases 1 to 642)
Sibbesen, O. and Soerensen, J.F.
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JP 2002533121-A/5.
synthetic construct
                                                    3D234187,1 GI:33043957
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Best Local Similarity 72.5%;
Matches 103; Conservative
                                                                                          JP 2002533121-A/4.
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SOERENSEN JENS FRISBAEK (DK); DANISCO (DK); SIBBESEN OLE (DK)
Location/Qualifiers
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/organism='Artificial Sequence'
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="wild-type xylanase"
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Sequence 6 from Patent WO0039289,
AX027172 GI:10188158
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1 (bases 1 to 642)
Sibbesen,O. and Soerensen,J.F.
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121 GGGGGTACCGTAAACGCTGTCA 142
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JP 2002533121-A/2.
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AX027172
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SOERENSEN JENS FRISBAEK (DK); DANISCO (DK); SIBBESEN OLE (DK)
Location/Qualifiers
                                                                                                                          Proteins
Patent: WO 0039289-A 10 06-JUL-2000;
SOERENSEN JENS FRISBAEK (DK) ; DANISCO (DK) ; SIBBESEN OLE (DK)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                    Query Match
44.2%; Score 79.6; DB 6;
Best Local Similarity 72.5%; Pred. No. 7.2e-16;
Matches 103; Conservative 0; Mismatches 39;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/noTe="mutant xylanase"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/nofe="mutant xylanase"
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Sequence 12 from Patent WO0039289.
                                                                                                               Soerensen, J.F. and Sibbesen, O.
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AX027176.1 GI:10188160
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AX027178
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Xylanase variants having altered sensitivity to xylanase inhibitors
Patent: WO 0166711-A 10 13-SEP-2001;
DANISCO A/S (DK)
Location/Qualifiers
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                                                                                                     1 ATGITTAAGTITTAAAAAAATTCTTAGTGGGATTTAACGGCAGCTTTCATGAGTATCAGC 60
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Bacillus subtilis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Bacillus subtilis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                   Length 642;
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                                 Query Match
43.9%; Score 79; DB 6; Length 642
Best Local Similarity 79.0%; Pred. No. 1.2e-15;
Matches 94; Conservative 0; Mismatches 25; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:1423"
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/mol type="unassigned DNA"
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Patent: WO 03020923-A 9 13-MAR-2003;
DANISCO A/S (DK)
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Sequence 9 from Patent W003020923.
AX717003.1 GI:29890250
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Sequence 10 from Patent WO0166711.
AX244979
AX244979.1 GI:15859704
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Best Local Similarity 79.0%; Pred. No. 1.2e-15;
Matches 94; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Oy 1 AIGITTAAGATTAAAAAGAATTCTTAGTGGGATTAACGGCAGCTTTCATGAGTATCAGC 60
Db 4 AIGITTAAGATTAATTCTTAGTGGGATTATCGGAGCTTTAATGAGTATTAGC 63
Oy 61 AIGITTTCTGCAACCGCCTCTGCAGCTGGATTAATGAGTATTAGC 63
Db 64 TIGITTTCTGCAACCGCCTCTGCAGCTAACACACATCACCATCACCATTAATGAGG 112
Db 64 TIGITTTCGGAACCGCCTCTGCAGCTAACACACACATCACCATCACCATTAGGATTGGATTGGATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGGAATTGAATTGGAATTGAATTGGAATTGAATTGGAATTGAATTGGAATTGAATTGGAATTGAATTGGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATTGAAT
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AGENCOURT AGENCOURT K-EST0176

Homo sapi AGENCOURT

AY414900 BM915836 AY414901 BM423896 CA487516 BM556479

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Homo sapiens (human)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 906)
NIH-MGC http://mgc.nci.nh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gappbe-remail: Kristi, A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov. i column: 15
High quality sequence stop: 712.
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BMS53432 AGENCOURT
BMS54035 AGENCOURT
BMS57421 AGENCOURT
                                                                                                                                      October 9, 2004, 00:53:40 ; Search time 3228.76 Seconds (without alignments) 4837.123 Million cell updates/sec
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BG54820 6C25752472
BG54820 6C25752472
BG54820 6C25752472
BM003247 6G3629663
CM113926 AGDACOURT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can btup://image.llnl.gov
http://image.llnl.gov
Plate: LLCN1968 row: p column: 03
High quality sequence stop: 746.
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; Pred. No. 7.9e-97;
0; Mismatches 0;
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/organiem="Homo sapiens"
/mol_type="mtNA"
/db_xref="taxon:9606"
/clone="IMAGE:5467250"
                                                                                                     Ph.D.
                                                                                                  Contact: Robert Strausberg, F
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Best Local Similarity 100.0%;
Matches 523; Conservative 0;
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/clone lib= MAPCL"
/note="Vector: pCMV-SPORT6; Site_1: BcoRV; Site_2: Not I;
Subtracted with brain, liver; lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
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hTERT-HME1, LNCaP"
/lab host="EMDH10B"
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.larity 100.0%; Pred. No. 7.3e-97;
Conservative 0; Mismatches 0;
                                                      organism="Homo sapiens"
                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:6719127"
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Matches 523; Conserv
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/organism="Homo sapiens"

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_6578800 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5466747
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( Dases 1 to 983)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1967 row: k column: 04
High quality sequence stop: 593.
Llocation/Cualifiers
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99.8%; Pred. No. 1.2e-96;
live 0; Mismatches 1;
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I (bases I 10123)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Concact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CONR Library Preparation: Rubin Laboratory
CONR Library Preparation: Rubin Laboratory
CONR Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: Mgc clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1974 row: a column: 19
High quality Sequence stop: 753.

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/lab host="nDH10B (phage-resistant)"
/lone="lorgan: RKIN; Vector: pOTB7; Site_1: XhoI; Site_2:
BCORI; CDNA made by oligo-dT priming. Directionally cloned
into BCORI/KhoI sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II TR (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                   1123 bp mRNA linear EST 20-FEB-2002
_6580951 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5469210
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                                                                                                                                                                                                                      BMS54035.1 GI:18793290
                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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5', mRNA Sequence.
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Location/Qualifiers

Losation/Qualifiers

Lorganism="Homo sapiens"

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="teaxon:9606"

/db_xref="teaxon:9606"

/clone lib="Single gene library"

/note="Vector: pbrive Cloning Vector; RT-PCR was performed using gene-specific primers flanking the open-reading frame. PCR products were subcloned into pbrive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencing using primers flanking the gapped areas."
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1 (bases 1 to 897)

Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R., Au-Young, J. and Stuve, L.L.

PCR isolation and cloning of novel splice variant mRNAs from known
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90136839 Single gene library Homo sapiens CDNA, mRNA sequence.
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99.7%; Score 521.4; DB 14; Length 897;
Best Local Similarity 99.8%; Pred. No. 1.5e-96;
Matches 522; Conservative 0; Mismatches 1; Indels 0;
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3160 Porter Drive, Palo Alto,
Tel: 650 621 8639
Fax: 650 621 8965
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Homo sapiens
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Unpublished (2003)
Contact: Jin, P.
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BM923410 1096 bp mRNA linear EST 12-MAR-2002
AGENCOURT 6625827 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5759022
5', mENA Sequence.
BM923410
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1. (Dassa: 1 to 1056)

1. NIH MGC http://mgc.nci.nih.gov/.

1. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM12803 row: m column: 07

High quality sequence stop: 646.
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Catarrhini, Hominidae, Homo.
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/note="Organ: pooled colon, kidney, stomach; Vector:
pcwv-SPORT6; Site_1: NOLI; Site_2: EcoRV (destroyed); ]
source anonymous pool of 3 colons, age 26 yo male, 49
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/db xref="taxon:9606"
/clone="IMAGE:5759022"
/lab_host="DH10B"
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Homo sapiens
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/organism="Homo sapiens"
// mol_type="mRNA"
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_6620268 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5590315
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LinL at: http://mage.lln.gov n.column: 11 Plate: LinM12363 row: n.column: 11 High quality sequence start: 10 High quality sequence stort: 599.
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       female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (ECGRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 624)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Suckville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Direct Submission
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                                                                        CTGGAGGTGTCGTACCGCGTTCTACGCC-ACCTTGCCCAGCCC
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM5378"
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//clone lib= NHT MGC 125"
//clone lib= NHT MGC 125"
//note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EccNV (destroyed); Site 2: Not1; RNA source pool
of three ovaries, from females ranging in age from 38 to
9 yo. Library is oligo-dT primed and directionally cloned
(ECCNV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
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                                                                                                                                                                                                                                                                                                      Contact: Strausberg, Ph.D.
Contact: Gapbs-remail.nih.gov
Tissue Procurement: Invitrogen
Tissue Procurement: Invitrogen
Tissue Procurement: Invitrogen
CDNA Library Praparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.ilnl.gov
Plate: LLAMA12364 row: g column: 20
High quality Sequence Stop: 513.
Location/Qualifiers
// organism="Homo sapiens"
// mol.type="mRNA"
// http:// column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Location/Column: Locat
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                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I Chases I to 1445)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/lab_host="DH108"
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11. "March Putp://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ontract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTT/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2048 row: n column: 10
High quality sequence stop: 542.
Location/Qualifiers
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                                                       ACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAG
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            Pred. No. 9.7e; Mismatches
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BM423896
BM423896.1 GI:18392108
EST.
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/db_xref="taxon:9606"
/clone="IMAGE:5517129"
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          97.68;
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                          Conservative
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          Best Local Similarity
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BM423896
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FEATURES

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/tissue_type="amelanotic melanoma, cell line"
/lab_host="ThioB (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: porB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into BcoRI/KhoI sites using the following 5 adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Garald M. Rubin (University of California,
Berkeley, using ZAP-cDNA synthesis kit (Stratagene) and
Supersoript II FT (Life Technologies). Note: this is a
NIH_MGC Library."
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AGENCOURT_10809149 MAPCL Homo sapiens cDNA clone IMAGE:6719006 5', mRNA sequence.
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1 (bases 1 to 986)

1 NH-WGC http://mgc.ndi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

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Tissue Procurement: Kristi A. Egland, Ira Pastan
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larity 97.5%;
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cDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: The I.M.A.G.B. Consortion

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Plate: LlaM14276 row: d column: 14

High quality sequence stop: 562.
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                                                                                                                                                                                                                                                                                                                                                                                        Score 485.6; DB 14; Length 986;
Pred. No. 3.5e-89;
"Mismatches 9; Indels 2;
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/clone lib="HIH MGC 41"
/clone lib="The made by oligo-dr priming. Directionally cloned into Ecorl/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript I RT (Life Technologies). Note: this is a NIH_MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1012)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Pred. No. 1.2e-88;
0; Mismatches 10;
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/ Jesuer type="Uterine"
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/ loote="Organ: Cervix, Vector: pCNS-D2; Site l: EcoRI;
/ site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intect mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digsstion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The converted colls E. coli Toplof* by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                       CB126975 554 bp mRNA linear EST 29-JAN-2003
K-EST0176151 C1SNU17 Homo sapiens cDNA clone C1SNU17-14-A07 5',
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Kur, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
LO Frontiar Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                         Korea Research Institute of Bioscience & Biotechnology 52 Boun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
Fax: +82-42-860-4409
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="ClSNU17-14-A07"
/sex="F"
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Location/Qualifiers
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AUTHORS
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Query Match 81.5%; Score 426; DB 14; Length 554; Best Local Similarity 100.0%; Pred. No. 4.38-77; Matches 426; Conservative 0; Mismatches 0; Indels

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Sequence 825, App Sequence 22, Appl

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US-10-09-792A-20
Sequence 20, Application US/10009792A
Sequence 20, Application US/10009792A
Sequence 20, Application US/20030153049A1
GENERAL INFORMATION:
APPLICANT: LEE, Sang-Yup
APPLICANT: LEE, SANG-YUD
TITLE OF INVENTION: ESCHBRICHIA COLI STRAIN SECRETING HUMAN
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
FILE REPERENCE: HYLEEGO.001APC
CURRENT APPLICATION NUMBER: US/10/009,792A
CURRENT FILING DATE: 2002-10-29
REICR FILING DATE: 2001-03-31
PRIOR FILING DATE: 2001-03-31
NUMBER OF SEQ ID NOS: 27
SOCTHANAR: FRAESEQ for Windows Version 4.0
SEQ 1D NO 20
LENGTH: 531
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llarity 100.0%; Pred. No. 1.6e-133;
Conservative 0; Mismatches 0;
7 US-10-411-012-1

7 US-10-410-913-1

7 US-10-044-090-825

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Maximum Match 100%
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APPLICANT: Yu, Zailin
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APPLICANT: Yu, Zailin
TITLE OF INVENTION: EFFECTS
FILE REFERENCE: ZYU-0603
CURRENT APPLICATION NUMBER: US/10/609,346
CURRENT APPLICATION NUMBER: US/06-26
PRIOR FILING DATE: 2003-06-26
PRIOR FILING DATE: 2002-07-01
NUMBER: OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
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llarity 100.0%; Pred. No. 1.6e-133;
Conservative 0; Mismatches 0;
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US-10-609-346-17
US-10-609-346-17
Sequence 17, Application US/10609346
Publication No. US20040063635A1
GENERAL INFORMATION:
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CTGTGCCACCCCGAGGAGCTGGTGCTCGCTCGGACACTCTCTGGGCATCCCCTGGGCCTCCC
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                                                                                                     CTGAGCAGCTGCCCCAGCCAAGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGC
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Sequence 18, Application US/10009792A

Publication No. US20030153049A1

GENERAL INFORMATION:
APPLICANT: LEE, SONG-YUP

APPLICANT: LEE, SCHERICHIA COLI STRAIN SECRETING HUMAN

TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING G-CSF)

FILE REFERENCE: HYLEGGO.01APC

CURRENT APPLICATION NUMBER: DCT/KR01/009,792A

CURRENT FILING DATE: 2001-0.29

PRIOR APPLICATION NUMBER: PCT/KR01/00549

PRIOR FILING DATE: 2001-03-31

PRIOR FILING DATE: 2001-03-31

NUMBER OF SCO ID NOS: 27

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 615
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US-10-009-792A-18
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APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Lee-Hwei X
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US-10-609-346-7
                                                                                       Sequence 7, Application US/10609346; Publication No. US20040063635A1; GENERAL INFORMATION:
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APPLICANT: Rafil, Shahin
APPLICANT: Hatcori, Koichi
APPLICANT: Hatcori, Koichi
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Adult Stem Cell Recruitment
FILE REFERENCE: 1676.066USI
CURRENT APPLICATION NUMBER: US/10/447,315
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: US 60/383,658
PRIOR APPLICATION NUMBER: 2002-06-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FELLSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 1498
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Publication No. US20040071687A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 3.2e-133;
Matches 522; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: hG-CSF-L-vFc gamma2 (Figure 2A)
US-09-968-362-17
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TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulaing factor; TITLE OF INVENTION: bloodgical activities; FILE REPERENCE: 03SUN2001 CURRENT APPLICATION NUMBER: US/09/968,362 CURRENT FILING DATE: 2001-10-30 NUMBER OF SEQ ID NOS: 22 SOFTWARE: Patentin version 3.1 SEQ ID NO 21 Lancount.
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ORGANISM: Artificial Sequence
FEATURE:
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GENERAL INFORMATION:

APPLICANT: Neose Technologies, Inc.

APPLICANT: DeFrees, Shawn

APPLICANT: APPLICANT: Robert

APPLICANT: Chen, Xi

TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE

TITLE OF INVENTION: WETHODS

TITLE OF INVENTION: METHODS

FILE REFERENCE: 040853-01-5053

CURRENT APPLICATION NUMBER: US 60/328,523

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR PILING DATE: 2001-10-19

PRIOR PILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR PELING DATE: 2002-06-25

PRIOR FILING DATE: 2002-07-17

PRIOR PLING DATE: 2002-07-17

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ilarity 99.8%;
Conservative (
LENGTH: 525
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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          ; LENGTH: 525
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Chen, Xi
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Publication No. US20040043446A1
GENERAL INFORMATION:
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Publication No. US20040077836A1

GENERAL INFORMATION:

APPLICANT: Neose Technologies, Inc.

APPLICANT: DeFrees, Shawn

APPLICANT: Bayer, Pobert

APPLICANT: Chen, Xi

APPLICANT: Chen, Xi

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Pred. No. 4.5e-133;
0; Mismatches 1;
                                  60/407,527
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SCOTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 525
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.8
Matches 522; Conservative
                                                                                                                                                                                                            TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-026-1
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APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: How, Xi
APPLICANT: TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: ALPHA
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Pred. No. 4.5e-133;
0; Mismatches 1;
PRIOR APPLICATION NUMBER: US 60/38/,22/
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PALENTIN PRIOR 175
SOFTWARE: PALENTIN PRIOR 13.2
LENGTH. 525
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Best Local Similarity 99.8%;
Matches 522; Conservative
                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-410-962-1
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FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR FILING DATE: 2003-04-09
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PILING DATE: 2002-06-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
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Publication No. US20040115168A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
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CRGANISM: Homo sapiens
US-10-411-049-1
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US-10-41L-016.-1

Sequence 1, Application US/10411012

Publication No. US20040122640A1

GENERAL INFORMATION

APPLICANT: Neose Technologies, Inc.

APPLICANT: Defrees, Shawn

APPLICANT: Defrees, Shawn

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Bovid

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: GLAYOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE

TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED

FILE REFERENCE: 040853-01-5051

CURRENT FILING DATE: 2003-04-09

PRIOR PLILOR DATE: 2001-10-10

PRIOR PLILOR DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR APPLICATION NUMBER: US 60/394,249

PRIOR PLILING DATE: 2002-06-17

PRIOR APPLICATION NUMBER: US 60/404,249

PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR APPLICATION NUMBER: US 60/407,527

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PRIOR APPLICATION NUMBER: US 60/407,527

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PRIOR PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR PRIOR PRIUM DATE: 2002-06-28
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Pred. No. 4.5e-133;
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SEQ ID NO 1
LENGTH: 525
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US-10-411-012-1
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Best Local Similarity
Matches 522; Conserv
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                                              US-10-410-997-1

US-10-410-997-1

Sequence 1, Application US/10410997

Publication No. US20040126838A1

GARDRAL INFORMATION:

APPLICANT: Neose Technologies, Inc.

APPLICANT: DeFrees, Shawn

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

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CORGANISM: Homo sapiens
US-10-410-997-1
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SIREE: TICK NORTH GLEER FORD
CUTY: VICE NORTH GLEER FORD
COMPUTER: VIRGINIA
COMPUTER READABLE FORM:
MEDIUM TYPE: Flory disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,411
FILING DATE: 03-MAY-1995
FILING DATE: 23-DEC-1986
PRICE APPLICATION DATA:
APPLICATION NUMBER: JP 51357/88
FILING DATE: 04-MAR-1988
ATTCRNEY/AGENT INFORMATION:
NAME: CRAWFORD, ARTHUR
REGISTRATION NUMBER: 25327
REGISTRATION NUMBER: 25327
REFERENCE/DOCKET NUMBER: 249-73
TELECOMMUNICATION INFORMATION:
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APPLICANT: SATO, MORIYUKI
APPLICANT: SATO, MORIYUKI
APPLICANT: ORABE, MASAMI
APPLICANT: ORABE, MASAMI
APPLICANT: TICH, SEIGA
APPLICANT: YAMASAKI, MOTOO
APPLICANT: YAMASAKI, MOTOO
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YOKOO, YOSHIHARU
APPLICANT: YOSHIDA, HALIME
APPLICANT: YOSHINORI, KOMATSU
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/08434411; Patent No. 5681720; GENERAL INFORMATION:
    RESULT 1
US-08-434-411-1
  13, Appli
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Copyright (c) 1993 - 2004 Compugen Ltd.
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STIMULATING FACTOR"
                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 110. C. C. COMPUTER: 110. C. COMPUTER: 110. SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURSENT APPLICATION NUMBER: US/08/434,402 FILING DATE: 03-MAY-1995 CLLASSIFICATION: DATA: APPLICATION NUMBER: US/08/99/86 FILING DATE: 23-DEC 1986 FILING DATE: 23-DEC 1986 FILING DATE: 13-MAR-1988 FILING DATE: 04-MAR-1988 FILING DATE: 04-MAR-1988 FILING DATE: 14-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 FILING DATE: 31-MAR-1988 F
                                                                                                   STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUWTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
   NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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Best Local Similarity 100.0%;

Matches 523; Conservative 0
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TYPE: nucleic acid
STRANDEDNESS: double
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MIYAJI, HIROMASA
SATO, MORIYUKI
OKABE, MASAMI
MORIMOTO, MAKOTO
ITOH, SEIGA
YAMASAKI, MOTOO
YOKOO, YOSHIHARU
YAMAGUGHI, KAZUO
YOSHIDA, HAJIME
YOSHIDA, HAJIME
YOSHINORI, KOMATSU
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Patent No. 5714581
GENERAL INFORMATION:
TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: 1.near
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1:522
LOCATION: 1:522
OTHER INFORMATION: STIMULATIIU
US-08-434-411-1
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Best Local Similarity 100.0%;
Matches 523; Conservative 0
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APPLICANT: YOSHINOR
TITLE OF INVENTION:
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                                                                                                                                                                                /product= "HUMAN GRANULOCYTE COLONY STIMULATING FACTOR"
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Best Local Similarity 100.0%; Pred. No. 5.5e-115;
Matches 523; Conservative 0; Mismatches 0;
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APPLICANT: YOSHIDA, HAJIME
ATITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
STREET: STREET:
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Patent No. 5994518
GENERAL INFORMATION:
APPLICANT: KUGA, TETSURO
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MIYAJI, HIROMASA
SATO, MORIYUKI
OKABE, MASAMI
MORIMOTO, MAKOTO
   STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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YAMASAKI, MOTOO
YOKOO, YOSHIHARU
YAMAGUCHI, KAZUO
                                                                                                                 ) NAME/KEY: CDS
; LOCATION: 1..522
; OTHER INFORMATION:
US-08-783-288-1
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COUNTRY: U.S.A.

ZID: 2201-4714

COMPUTER READABLE FORM:
MEDIUM TYRE: IBM PC COMPATIBLE
COMPUTER: EMPLY OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE OF GREAT STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE 
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APPLICANT: MIYAJI, HIROMASA
APPLICANT: SATO, MORITUKI
APPLICANT: MORINOTO, MAKOTO
APPLICANT: TOWASE MASANI
APPLICANT: YAMASAKI, MOTOO
APPLICANT: YAMASAKI, MOTOO
APPLICANT: YAMAGUCHI, KAZUO
APPLICANT: YOKNIDA, HAJIME
APPLICANT: YOSHIDA, HAJIME
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APPLICANT: YOSHIDA, HAJIME
APPLICANT: YOSHIDA, HAJIME
SAFRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CITY: 1100 v.
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Patent No. 5795968
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TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 Dase
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5194592-25
; Patent No. 5194592
; Patent LONINE YOSHIDA, HAJINE
; POLYPEPTICANT: YOSHIDA, HAJINE
; POLYPEPTIDES DERIVITUES OF HUMAN GRANULOCYTE COLONY
; STIMULATING FACTOR
; NUMBER OF SEQUENCES: 83
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/318,527
; FILLING DATE: 3-MAR-1989
; PRIOR APPLICATION NUMBER: 136,647
; FILLING DATE: 22-DEC-1987
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100.0%; Score 523; DB 6; L
Best Local Similarity 100.0%; Pred. No. 5.5e-115;
Matches 523; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 523; DB 2; Length 5
Best Local Similarity 100.0%; Pred. No. 5.5e-115;
Matches 523; Conservative 0; Mismatches 0; Indels
     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FRATURE:
NAME/KEY: CDS
LOCATION: 1..525
OTHER INFORMATION: /produce=OTHER INFORMATION: STIMULATI
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Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Jung, Patrice
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
CONTAINING SAID POLYPEPTIDES
                                                                                               311
                                                                                                                                            CCCACCTTGGACACACTGCAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAG 360
                                                                                                                                                                                     312 eccaectrigaacacactricaactricatericaccactriricacacacatericacacacad
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           192 CTGAGCTCCTGCCCCAGCCCAGGCCCTGCAGCTGGCAGCTTGAGCCAACTCCATAGC 251
                                                                              252 GGCCTTTTCCTCTACCAGGGCTCCTGCAGGCCCTGGAAGGGATTCCCCCCGAGTTGGGT
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COMPUTER: Macintosh
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COMPUTER: Macintosh
CORFWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-0Ct-2001
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INCORMATION:
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INCORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/09984186
Patent No. 6686179
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
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ZIP: 19426
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-P
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Sequence 13, Application US/08797689
Fatent No. 587696
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Veh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CCTTLE COLlegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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Pred, No. 5.9e-112;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19426
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
NAME: Smith Ph.D., Julie K.
NAME: Smith Ph.D., Julie K.
PROSENTATION NUMBER: P.38, 200065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: $192006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.5%;
Matches 515; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 541 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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US-08-797-689-13
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1853 Accecerressecretes as a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contract and a contrac
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Best Local Similarity 98.5%; Pred. No. 8.2e-112;
Matches 515; Conservative 0; Mismatches 8;
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/256,938
FILING DATE: US/08/256,938
PRICATION: 435
PRICA APPLICATION DATA:
APPLICATION NUMBER: FF 92/01065
FILING DATE: 31-JAN-1992
ATTORNEY FAGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE DOORMAN EAST NUMBER: ST92007-US
TELEPANTION FOR SEQ ID NO: 1:
TELEPANTION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2382 Base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRRANDENNESS: Gouble
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LOCATION: 18427.1848
OTHER INFORMATION: /label= MstII-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; LOCATION: 2035_2040; OTHER INFORMATION: /label= SstI-site US-08-256-938-1
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OTHER INFORMATION: /label= Apal-site
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LOCATION: 1861..1866
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND TITLE OF INVENTION: PRARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES NUMBER OF SEQUENCES:
I TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 50 Arcola Road, 3C43
CITY: Collegeville
STRIET: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.0 (Patentin)
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                                                                                                                                                , NAME/KEY: CDS
; LOCATION: 3..536
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-984-186-13
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Patent No. 5665863
                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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US-08-256-938-1
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TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEDE: Rhone-Poulenc Roger Inc.
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                                                                                                                             Query Match 97.4%; Score 509.2; DB 1; Length 2455; Best Local Similarity 98.5%; Pred. No. 1.4e-111; Matches 514; Conservative 0; Mismatches 8; Indels 0;
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; LOCATION: 620..631
; OTHER INFORMATION: /label= polyGly-linker
US-08-256-938-3
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Patent No. 5876569
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Yeh, Patrice
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Collegeville
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COMPUTER: Macintosh
OPERATING SYSTEM: SYSTEM 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797.64
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08256938

Batent No. 5665863

GENERAL INFORMATION:
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CCITY: Collegeville
STATE: PA
CCUNTRY: USA
2273 GCCTCTGCTTTCCAGCGCCGGGCAGAGGGTCCTGGTTGCTAGCCATCTGCAGAGCTTC 2332
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REGISTRATION VMBBE: 32,534
REFERENCE/DOCKET NUMBER: $792007-US
TELECOMUNICATION INPORMATION:
TELEPANE: (610) 454-3817
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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LOCATION: 2376..2382
OTHER INFORMATION: /label= MstII-site
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NAME: Misc_feature
NAME: 106.111
OCHER INFORMATION: /label= Apal-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
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TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 26..97
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26..2389
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MOLECULE TYPE: CDNJ
HYPOTHETICAL: NO
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LOCATION:
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NAME/KEY:
                                                                                                        481
                                                                                                                                                                   2333
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GENERAL INFORMATION:

GENERAL INFORMATION:

Pournier, Alain

Guitton, Jean-Dominique

Jung, Gerard

Yeh, Patrice

TILE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION

CONTAINING SAID POLYPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Greadgaagarccaggccaargccgcagcgcrccaggagaagcrerereccaccaacaac
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ZIF: 19426
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER Macintoon
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-OCt-2001
CLASSIFICATION: GURNOMA-
PRIOR APPLICATION: GURNOMA-
PRIOR APPLICATION NUMBER: US/09/984,186
FILING DATE: 31-JAM-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: PT/FR93/00085
FILING DATE: 31-JAM-1993
ATTORNEY/AGRATION:
NAME: Smith Ph.D., Julie K.
REFERENCE/DOCKET NUMBER: ST92006-US
TELEPAX: (610) 454-3809
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2455 basis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 509.2; DB 4;
Pred. No. 1.4e-111;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
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) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-984-186-15
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Best Local Similarity 98.5%;
Matches 514; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 Greadgaagarccageecgareececaececreccagaaacrererecaecaac
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                                                     FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
PROGRA APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATJORNEY/AGENT INFORMATION:
NAME: SEATE Ph.D., JULIE K.
REGISTRATION NUMBER: P-38,619
REGISTRATION NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
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US-09-984-186-15
; Sequence 15, Application US/09984186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.5%;
Matches 514; Conservative 0
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26..2389
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LOCATION:
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                                                                                          TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY: Fred Hutchinson Cancer Research Center
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96.9%; Score 507; DB 3;
Best Local Similarity 98.1%; Pred. No. 3.3e-111;
Matches 513; Conservative 0; Mismatches 10;
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FILING DATE:
PRELICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                              POSITION IN GENOME:
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MAP POSITION:
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LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
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JOURNAL:
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PILING DATE: 8.0" (6.71824-1993)

PILING DATE: 27-Jul-1993

ATTORIEXTA AGENT THRORMATION: NAME: OSTER, USG8/097,869

FILING DATE: 27-Jul-1993

ATTORIEXTA AGENT THRORMATION: NAME: OSTER, USG8/097,869

REGISTRATION NUMBER: 32,585 and 36,131, respectively TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Cell Therapeutics, Inc.
TREET: 200 Elliott Avenue West, Suite 400
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08149101A
Patent No. 6171824
GENERAL INFORMATION:
APPLICANT: Todaro, George J.
APPLICANT: Leung, David W.
APPLICANT: Rose, Timothy M.
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 26
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: homo sapien
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US-08-468-609A-177
US-08-468-609A-177
Sequence 177, Application US/08468609A
Patent No. 6030812
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
HAPPLICANT: Braford-Goldberg, Sarah R.
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Pred. No. 3.3e-111;
0; Mismatches 10;
                                                                GENERAL INFORMATION:

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COMPUTER: AST-IBM COMPATIBLE
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COMPATION SYSTEM: MS-DOS Version 6
SOFTWARE: WORD for WINDOWS
CURRENT APPLICATION DATA:
INFORMATION FOR SEQ ID NO: 1:
APPLICANTON FOR SEQ ID NO: 1:
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US-08-469-318-177
; Sequence 177, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
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Best Local Similarity 98.1%;
Matches 513; Conservative
                                                  PCT-US94-12873-1
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TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis in TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARIE: Patentin Release #1.0, Version #1.30 (EPG SOFTWARY APPLICATION DATA: APPLICATION NUMBER: US/08/469,318
FILING DATE: PATENTION: PRIOR APPLICATION NUMBER: 08/446,872
FILING DATE: FLING DATE: FLING DATE: FLING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: TELING DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE:
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GCCTCTGCTTTCCAGCGCCGGGCAGGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTC 480
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Job time : 83.3471 secs
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APPLICANT: Caparon, Maire H.
APPLICANT: Easton, Alan M.
APPLICANT: Milen, Barbara K.
APPLICANT: Milen, Barbara K.
APPLICANT: Morearn, John P.
APPLICANT: Olins, Peter O.
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                      COMPUTER: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
FILING DATE: 06-UUN-1995
PRIOR APPITCATION:
                                                                                                                                                                                                           3: Dennis A. Bennett, G.D. Searle & Co.
3: Corporate Patent Dept.
P. O. Box 5110
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APPLICATION NUMBER: US 08/192,325
FILING DATE: 14 FEB-1994
ATTORNEY AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/3
TELECOMMUNICATION INFORMATION:
TELEFAX: (314)737-696
TELEFAX: (314)737-696
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 base pairs
TYPE: nucleic acid
STRANDENDESS: Gouble
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MOLECULE TYPE: DNA (genomic)
US-08-468-609A-177
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Best Local Similarity 97.7%;
Matches 511; Conservative
                                                                                                                                                                                                           ADDRESSEE: Dennis
ADDRESSEE: Corpor
STREET: P. O. BOX
CITY: Chicago
STATE: Illinois
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pMON13063 pMON13152 Human int Human int pMON13045

Human int

RESULT 1

ALIGNMENTS

AAN80947 standard; DNA; 525 BP (first entry) 15-NOV-1990 AAN80947;

Granulocyte colony stimulating factor; hG-CSF; macrophage; tumour therapy; leŭkaemia; ss.

87EP-00119157. `. . 23-DEC-1987; 29-JUN-1988 EP272703-A.

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Pred. No. is the number of res score greater than or equal to and is derived by analysis of

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genesequ2003bs:*
genesequ2003bs:*

SUMMARIES

Sato M, Miyaji H, (KYOW) KYOWA HAKKO KOGYO KK Komatsu Y, Yamasaki M; Kuga T, Itoh S,

WPI; 1988-176825/26 P-PSDB; AAP80965 The sequence is carried on plasmid pCSF1-2 isolated from a cDNA library prepared from mRNA extracted from peripheral blood macro- phages. It encodes a protein whose AA sequence agrees with those determined for G-cSF from the human squamous cell line CHU-II and the human bladder cancer cell line 5637. It can be used as a "master gene" for the construction of mutant genes which encode variants of hG-CSF which differ by at least one AA. See also AAN80945 and AAN80946

Sequence 525 BP; 85 A; 192 C; 151 G; 97 T; 0 U; 0 Other;

AAN8094

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseq 29Jan04:*

Database

geneseqn1980s:* geneseqn1990s:*

G-CSF gene isolated from peripheral blood macrophages

Homo sapiens.

86JP-00306799. 23-DEC-1986;

G-CSF gen Human hG-Human hG-Plasmid p Sequence

Description

OB

Score

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Aan80947

Plasmid p Sequence

AAN71320 AAN60937 AAN81478

AAD19771 AAN70223 AAN80947

AAN91086 ACC78869 ABA94177

Plasmid p

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Human gra Human gra CDNA enco

Aaq24283 Aaf56684 D Aaq87151 D Abk68973

IL-3:G-CS

Σ

Morimoto

Okabe M,

Human granulocyte colony stimulating factor polypeptide derivs. - having at least one different aminoacid, giving high specific activity and stability.

Disclosure, Page ?; 68pp; English.

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AAD19771 standard; DNA; 615
               WPI; 2001-616523/71.
P-PSDB; AAE12154.
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Xa; kanamycin resistance; endoxylanase signal peptide; ds
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                               The invention relates to an Escherichia coli producing and secreting human granulocyte colony stimulating factor (hG-CSF), more specifically, to a recombinant plasmid constructed to express secretory hG-CSF in E. coli, an E. coli transformed with that plasmid to secrete hG-CSF, and a process for preparing hG-CSF using the transformed hG-CSF. The recombinant plasmid vector comprises of a kanamycin resistance gene, a promoter, an endoxylanase signal sequence, a nucleotide sequence coding for an olioopeptide consisting of 13 amino acids including 6 consecutive historian residues and a hG-CSF. E. coli transformed with recombinant plasmid vector is useful for preparing hG-CSF. The method comprises culturing the microorganism to obtain a hG-CSF fusion protein and treating the fusion protein with a protease preferably Factor Xx, to obtain a hG-CSF, where the fusion protein is obtained from the culture by employing Ni-column. The present sequence is human hG-CSF gene inserted
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                           human granulocyte colony stimulating factor gene and other components, when transformed into microorganism useful for preparing the colony
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Recombinant plasmid vector comprising an endoxylanase signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 531 BP; 89 A; 192 C; 151 G; 99 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGAGGTGTCGTACGCGTTCTACGCCACCTTGCCCAGCCCT
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ilarity 100.0%; Pred. No. 2.2e-107;
Conservative 0; Mismatches 0;
                                                                                                                                                           Example 2; Fig 5; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  into plasmid pEDCSFm
                                                                                             stimulating factor.
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Best Local Simil
Matches 523; (
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us-10-009-792c-18_copy_88_610.rng

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CCCACCTTGGACACACTGCAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAG 360
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208 CTGTGCCACCCCGAGGAGCTGGTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poly:peptide with human granulocyte colony stimulating factor activity is obtd. by cultivating transformant formed by recombinant DNA procedures.
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                                                                                                                328 geccrirircciciaecaecaccicidadecaeccineaaeceaicicceceaericee
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                            CTGAGCAGCTGCCCAGCCAAGCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATAGC
                                                                                     GGCCTTTTCCTCTACCAGGGCTCCTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human granulocyte colony stimulating factor; G-CSF; leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                              CTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCT 610
                                                                                                                                                                                                                                                                                                                           CTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCT 523
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31. .645
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85JP-00217150.
85JP-00269455.
85JP-00269456.
85JP-00270838.
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86JP-00166709
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pBRV2 insert.
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P-PSDB; AAP70162.
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30-SEP-1985;
02-DEC-1985;
02-DEC-1985;
03-DEC-1985;
03-DEC-1985;
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25-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant plasmid vector comprising an endoxylanase signal sequence, human granulocyte colony stimulating factor gene and other components, when transformed into microorganism useful for preparing the colony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GIGAGGAAGAICCAGGGCGAIGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG
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                                                                                                       granulocyte colony stimulating factor; hG-CSF; protease; Xa; kanamycin resistance; endoxylanase signal peptide; ds.
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                                                                                                                                                                                     88. .612
/*tag= a
/*tag= a
/*toduct= "Human hG-CSF protein"
/note= "CDS does not include start codon"
/partial
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100.0%; Pred. No. 2.2e-107;
ive 0; Mismatches 0;
                                                                          gene inserted into plasmid p19CSFm.
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                                                                                                                                                                              location/Qualifiers
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                                                (first entry)
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Best Local Similarity 100.
Matches 523; Conservative
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P-PSDB; AAE12153.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee S, Jeong K;
                                                                                                                                                                                                                                                                                     WO200173081-A1
                                                                              Human hG-CSF
                                                                                                                                                     Homo sapiens
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AAN60937 standard; DNA; 1521
                                                                                           (CHUS ) CHUGAI SEIYAKU
                                                                                                                Nomura H,
                                                                                                                                     WPI; 1987-095431/14.
P-PSDB; AAP71384.
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 523; Conserv
                                         3-OCT-1986;
                                                             04-OCT-1985;
02-JUN-1986;
                    08-APR-1987
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                The plasmid was isolated from a cDNA library prepd. from CHU-2 cells, human oral cavity tumour cell line, using a 1500 bp insert from pBRG4 (AANY0222) and probe LC (AANY1351). The plasmid was used to prepare recombinant expression plasmids for the prodn. of h G-CSF. See also AANY0221-N70224 and AANY1351. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence encoding human granulocyte colony stimulating factor (hGCSF)
                                                                                                                                      Gaps
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                                                                                                                 Length 1520;
                                                                                            Sequence 1520 BP; 303 A; 487 C; 402 G; 328 T; 0 U; 0 Other;
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                                                                                                               Score 523; DB 1; L
Pred. No. 2.5e-107;
; Mismatches 0;
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31. .120
English
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larity 100.0%;
Conservative 0
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121. .645
/*tag= b
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4; 73pp;
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Best Local Similarity
Matches 523; Conserv
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Disclosure;
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                                                                                                                                                                                                                                                                              Leukopenia treating agent esp. for producing fully mature neutrophiles -contains human granulocyte colony stimulating factor obtd. by recombinant DNA methods etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The hGCSF has the following properties: (i) mol. wgt. 19000 +/- 1000 (by SDS-PAGE); (ii) isoelectric pt. at 5.5, 5.8 or 6.1 each +/- 0.1, (iii) UV max. absorption at 280nm and min. at 250nm. Prodn. of the gene, vector etc. is described in UP 269455, 269456, 270838 and 270839, each of 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 ATGGAAGAACTIGGGAATIGGCCCCTGCCCTGCACCCACCCAGGCTGCCATGCCGGCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1520 BP; 305 A; 488 C; 401 G; 326 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                523
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                                                                                                                                                                          Ë
                                                                                                                                                                          Ouo
                                                                                                                                                                          ĸ,
                                                                                                                                                                             Hattori
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Fig 2; 34pp; English.
86EP-00113671
                                             85JP-00220450
86JP-00125660
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523

420

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Human recombinant granulocyte colony-stimulating factor - causes differentiation of granulocytes and monocytes from bone marrow progenitor
                                                                            CCCACCTTGGACACACAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAG 480
                                                                                                                                                                                                                                                             Sequence encoding human granulocyte colony-stimulating factor (G-CSF) in clone pP12 of MIA PaCa cDNA library.
                                         421 eccreteracratices acces acces acces acces acces acces acces acces.
                       ATGGAAGAACTGGGGAATGGCCCTGCCTGCAGCCCAACCCAGGGTGCCATGCCGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The major difference between this clone and the CHU-2 cDNA clones of Nagata et al. (EMBO Journal 5:3,575-581(1996)) are given in FT of AAN81478. The G-CSF was detected in purified mRNA fraction obtd. by
                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
133. .657
/*tag= b
237. .238
/*toc= "CHU-2 cDNA clones of Nagata et al. contains
base pair insertion (GTGATGGAG)"
                                                                                                                                                                                                                                                                                            Leukaemia therapy; anaemia treatment; leukocyte; lymphokine;
interleukin-3; ss.
                                                                                                                       CIGGAGGIGICGTACCGCGTTCTACGCCACCTTGCCCAGCCCT 643
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"C in the CHU-2 clone"
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"G in the CHU-2 clone"
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                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                        AAN81478 standard; cDNA; 1525
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86US-00932037.
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(first entry)
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/note=
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/note=
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P-PSDB; AAP81162.
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18-NOV-1986;
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14-DEC-1990
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                                                                                                                                                                                                               AAN81478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The plasmid encodes a novel polypeptide having human graulocyte colony stimulating factor activity. The CSF may be produced either from a cellline secreting the factor into its medium, or from a transformant microorganism. The product induces high immunity to infection by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIGIGECACCCCGAGGAGGAGCTGGTGCTCGGACACTCTGGGCATCCCCTGGGCTCCC
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stimulating factor obtd. by cell culture or recombinant technology
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                                                                                 G-CSF; granulocyte colony stimulating factor; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 523; DB 1; Length 1:
100.0%; Pred. No. 2.5e-107; Mismatches 0; Indels
                                                               Plasmid pBRV2 insert encoding granulocyte CSF
                                                                                                                                                                                                                                                                                                                            Matsumoto M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anaerobic and aerobic bacteria and fungi
                                                                                                                              Location/Qualifiers
31. .645
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 4; 139pp; Japanese.
                                                                                                                                                                                                                                                            85JP-00023777.85JP-00270839.
                                                                                                                                                                                                                                                                                                                              Tamura M,
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nes 523; Conservative
                                                                                                                                                                                                                                                                                                                                                   WPI; 1986-225384/34.
                                                                                                                                                                                                                                                                                                                               Nomura H,
                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAP61341
                                                                                                                                                                                                                                                                                              (CHUS ) CHUGAI (ONOM/) ONO M.
                                                                                                                                                                                                                                         07-FEB-1986;
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03-DEC-1985;
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Recombinant Baculovirus transfer vectors - used for prodn. of ocstimulating factor in Baculovirus-insect cell expression system.
                                                Martin G,
                                                                                                                                  Disclosure; Fig 3; 68pp; English
     87US-00077188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC78869 standard; DNA; 525
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                                                37,
                                               Devlin
                                                                    WPI; 1989-061174/08
                           CORP.
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                                                Kawasaki
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                                                                                                                                                  GTGAGGAAGATCCAGGGCGATGGCGCCTCCAGGAGAAGCTGTGCCACCTACAAG
                                                                                                                                                                 GTGAGGAAGATCCAGGGCGATGGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG
sucrose density gradient centrifugation of induced MIA PaCa-2 cells as described in WO8804607. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                              CTGTGCCACCCCGAGGAGCTGGTGCTCCTCGGACACTCTCTGGGCATCCCCTGGGCTCCC
                                                                                                                                                                                                                                                            CTGAGCAGCTGCCCAGCCCTGCAGCTGCAGCTGCTTGAGCCAACTCCATAGC
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                                                                  Length 1525
                                           Sequence 1525 BP; 303 A; 491 C; 402 G; 329 T; 0 U; 0 Other;
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                                                                ; Score 523; DB 1; I
; Pred. No. 2.5e-107;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colony stimulating
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                                                               100.0%;
ilarity 100.0%;
Conservative 0;
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                                                                          Best Local
Matches
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The cDNA insert of pP12 contains 11 more bases than the CHU-2 G-CSF clone. The major difference between this clone, derived from MIA PaCa-2, and CHU-2 clone is a 9 bp insertion in the CHU-2 clone between bases 237 and 238. There are two other differences: an A at position 588 (G in the CHU-2 clone) is a silent third base change, and a T at position 1237(C in the CHU-2 clone) in the 3' untranslated region. See also AAN91085
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                                                                                                                                                                                                                  Sequence 1525 BP; 303 A; 490 C; 403 G; 328 T; 0 U; 1 Other;
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P-PSDB; ABR55839.
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                                                                28-AUG-2002;
                                           10-OCT-2001;
                                             19-OCT-2001;
28-NOV-2001;
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                                               GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG
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/product= "G-CSF"
/note= "no start codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACCCCCTGGGCCCTGCCTGCTCCTGCCCAGAGCTTCCTGCTCAAGTGCTTAGAGCAA
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                                    Peptide remodeling; glycoconjugation; glycosyltransferase; glycan; granulocyte colony stimulating factor; G-CSF; human; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen X;
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/*tag= a
/product= "G-CSF"
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2002US-0391777P.
2002US-0404249P.
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The examples describe procedures for the designing of probes for hpG-CSF cDNA and genomic clones, both of which are claimed. Specifically claimed are DNA sequences encoding for (Ala 1)hpG-CSF, (Ser 36, 42, 64 and 74)hpG-CSF and the corresponding Met.1 cpds. The novelty is that hpG-CSF is the prod. of procaryotic or eucaryotic expression of an exogenous DNA described in the examples. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG
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                                                                                                                                                          85US-00768954.
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86US-00835548.
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Best Local Similarity 99.8%;
Matches 522; Conservative
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P-PSDB; AAP70730.
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                                               The present invention describes a recombinant microorganism expressing a granulocyte colony stimulating factor (G-CSF), and process for preparing the recombinant protein. The present sequence encodes a G-CSF related protein, which is given in the exemplification of the present invention
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                                                                                                                                                                         Query Match 99.7%; Score 521.4; DB 3; Best Local Similarity 99.8%; Pred. No. 5e-107; Matches 522; Conservative 0; Mismatches 1;
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Sequence 1508 BP; 294 A; 484 C; 402 G; 328 T; 0 U; 0 Other;

http.segdata.uspto.gov/sequence.html?DocID=20020137081

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                                                                                                                                                                                                                                                      Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant; hypotensive; antidiabetic; gynaecological; vascuropic; cerebroprotective; gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis; schaemia-reperfusion injury; stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated
                                                                                                                                                                                                                            Human cDNA #825 differentially expressed in activated vascular tissue.
                                CTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCT 559
                 CIGGAGGIGICGIACCGCGTTCIACGCCACCTIGCCCAGCCCT 523
                                                                                                                              ABX63825 standard; cDNA; 1508 BP
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08-JAN-2001; 2001US-0260483P.
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    Score 521.4; DB 7;
Pred. No. 5.6e-107;
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94. .621
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        Query Match
Best Local Similarity 99.8
Matches 522, Conservative
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//rag= b
//rag= "this part of the sequence encodes a 4 amino acid
poptide not present in the wild type protein"
64..66
/*tag= c
//note= "alternatively IGC at this position is replaced by
GCC causing an Ala residue to replace Cys in the protein"
                                                                                                                               /product= "recombinant human G-CSF"
/transl except= (pos:13. .15,aa.Xaa)
/note= "Xaa represents nothing i.e. nothing is given in
the protein at this position"
           colony stimulating factor; G-CSF; rhG-CSF;
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1. .540
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P-PSDB; AAY29929.
             granulocyte
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Best Local Similarity
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Synthetic.
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                                                                                                                                             The invention relates to a method for producing recombinant human granulocyte colony stimulating factor (rhGCSP). The method includes the following steps: (a) reverse transcription-polymerase chain reaction of the human granulocyte colony stimulating factor gene; (b) transforming bechericals coli; (c) renaturation of protein by hollow fibre ultrafiltration dialysis; (d) passing the renatured protein through ion exchange chromatography, hydrophobic chromatography and molecular sieve purifying so to obtain a high yield of high-purity medicinal rhG-GSF protein. The present sequence encodes rhG-GSF
                                                                                                                                                                                                                                                                                                                                                                                                               9
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0
                                                                                        stimulation
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                                                                                                                                                                                                                                                                                                                     Sequence 644 BP; 128 A; 216 C; 172 G; 128 T; 0 U; 0 Other;
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                                                                                   Production of recombined human granulocyte colony
                                                                                                                                                                                                                                                                                                                                                 98.2%; Score 513.4; DB 5; 98.9%; Pred. No. 3.1e-105; iive 0; Mismatches 6;
                                                                                                                   Disclosure; Page 8 (disclosure); 15pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
           Wang
                                        2001-590346/67.
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Matches 517; Conserv
                                                     P-PSDB; AAM51536
           Kong T,
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           Su Y,
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Colony stimulating factor for recombination of human granulocytes - obtained by adding 3-6 amino acid residues at N end of its sequence, which at least one amino acid residue is arginine.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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360 360 420 420 480 480

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PAT 29-SEP-1997
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04-NOV-1988
23-DEC-1987 JP 1987326384
23-DEC-1986 JP 86P 306799
KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E01731.1 GI:2169984

UP 198826722-A/1.

Homo sapiens (human)

Homo sapiens (human)

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 525)

Kuga,T., Yamazaki,M., Yokoo,Y. and Yamaguchi,K.

Itou,S., Yamazaki,M., Yokoo,Y. and Yamaguchi,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAMAGUCHI KAZUO
C12P21/02,C07K13/00,C12N1/20,C12N15/00//A61K37/02,A61K37/02,
                                                                               GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAGCTGTGTGCCACCTACAAG
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                            ACCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAGCAA
                                                               GTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAGCTGTGCCACCTACAAG
                                                                                                                    CTGTGCCACCCCGAGGAGCTGGTGCTCGGACACTCTCTGGGGCATCCCCTGGGCTCCC
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CDNA encoding hG-CSF form human periferal macrophage.
E01731
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NI MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO,
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Key Location/Qualifiers
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KYOWA HAKKO KOGYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (C12P21/02,C12R1:91);
strandedness: Double;
topology: Linear;
hypothetical: No;
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Unknown.
Unknown.
Unclassified.
I (bases I to 525)
I (bases I to 525)
Yamasaki, M.; Yokoo, Y., Yamaguchi, K., Yoshida, H. and Komatsu, Y.
Yamasaki, M.; Yokoo, Y., Yamaguchi, K., Yoshida, H. and Komatsu, Y.
Method of producing a polypeptide having human granulocyte colony
stimulating factor activity
Patent: US 599418-A 1 30-NOV-1999;
Location/Qualifiers
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100.0%; Score 523; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 523; Conservative 0; Mismatches 0;
                                                                                             100.0%; Score 523; DB 6;
llarity 100.0%; Pred. No. 2.5e-86;
Conservative 0; Mismatches 0;
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/organism="unknown"
/mol_type="unassigned DNA"
US 5795968-A 1 18-AUG-1998;
Location/Qualifiers
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Sequence 1 from patent US 5994518.
AR091731 GI:10018485
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/organism="unknown"
/mol_type="unassigned"
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PAT 29-SEP-1997
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                                                                                             C12N15/58,C12N15/70,C12N15/85,C12P21/02,C12P21/02,(C12N1/21,
                               C12N9/72, C07K13/00, C07K15/14, C12N1/21, C12N5/10, C12N9/64, PC
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100.0%; Score 523; DB 6; Length 5
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 523; Conservative 0; Mismatches 0; Indels
                                                                                                                         C12R1:19),
(C12P21/02,C12R1:19),(C12P21/02,C12R1:91);
strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
*source: cell_typelympnoblast LukII;
*source: clone=pCSF-2;
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1. .525
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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CDNA encoding human G-CSF.

E07164 1 GI:2175311

UP 1994092994-A/1.

Homo sapiens (human)
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E 1 (bases 1 to 525)
Sasaki,K., Nishi,T., Yasumura,S., Sato,M. and Itou,S.
NEW POLYBEPTIDE
L Patent: JP 1990227075-A 1 10-SEP-1990;
KYOWA HAKKO KOGYO CO LID
OS HOMO sapiens (human)
PN 1990227075-A/1
PD 10-SEP-1980 JP 1989253097
PR 28-SEP-1989 JP 1989253097
PR 29-SEP-1988 JP 88P 245705
PI SASAKI KATGUTOSHI, NISHI TATSUYA, YASUMURA SHIGEYOSHI, PI SATO MORIYUKI,
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peptide 1. .525
/product='mature peptide of hG-CSF'
Location/Qualifiers
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Pred. No. 2.5e-86;
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    .525
    /organism="Homo sapiens"
/mol type="genomic RNA"
/db_xref="taxon:9606"

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JP 1990227075-A/1.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 523; Conservative
      mat_peptide
      FT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MORIMOTO MAKOTO, ITOU SEIGA, YAMAZAKI MOTOO, YOKOO YOSHIHARU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YAMAGUCHI KAZUO
CO7K14/535,C12N1/21,C12N15/09,C12P21/02//A61K38/00,(C12N1/21,
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100.0%; Score 523; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 523; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
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(C12P21/02,C12R1:19);
strandedness: Single;
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                                                                                                                                                                     cDNA encoding hG-CSF. E09431
                                                                                                                                                                                                      E09431.1 GI:22026058
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Homo sapiens (human)
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YAMAGUCHI KAZUO
CO7K13/00,A61K37/02,C12N1/21,C12N15/27,C12P21/02,(C12N1/21, PC
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                                                         Kuga, T., Komatsu, Y., Miyaji, H., Sato, M., Okabe, M., Morimoto, M., Itou, S., Yamazaki, M., Yokoo, Y. and Yamaguchi, K. Namazaki, M., Yokoo, Y. and Yamaguchi, K. Namazaki, M., Yokoo, Y. and Yamaguchi, K. Namazaki, M., Yokoo, Y. and Yamaguchi, K. Namazaki, M., Yokoo, Y. and Yamaguchi, K. Namazaki, M. Os. Homo sapiens (human)

Ph. 1994092094-A/1

Ph. 1994092294-A/1

Ph. 1994092294-A/1

Ph. 23-DEC-1986 JP 1992214376

Ph. 23-DEC-1986 JP 86P 306799

Ph. KUGA TETSUO, KOMATSU YUKI, MIYAJI HIROMASA, SATO MORIYUKI, PI
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                  Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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l. :525
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Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 523; Conservative 0; Mismatches 0;
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    Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 525)
                                                                                                                                                                                                                                                                                                                               strandedness: Double;
topology: Linear;
hypothetical: No;
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(C12P21/02,C12R1:19);
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Ouery Ma Dest Loc Matches Qy Db
mar_peptide 1522 FT_Location/Qualifiers Source 1525 A525 A520 Arganism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" Query_Match 100.0%; Score 523; DB 6; Length 525;

Db 361 ATGGAAGAACTGGGAATGGCCCTGCCCTGCAGCCCACCCA	REFERENCE 1 (bases 1 to 525) AUTHORS Yoshida.H. TILLE Monoclonal antibodies to novel polypeptide derivatives of human granulocyte colony stimulating factor JOURNAL Patent: US 5194592-A 25 16-MAR-1993; FEATURES 1.0525 Source /organism="unknown" /mol_type="genomic DNA" ORIGIN ORIGIN 100.0%: Score 523; DB 6; Length 525;	Best Local Similarity 100.0%; Pred. No. 2.85-86; Indels 0, Gaps 0; Matches 523; Conservative 0; Mismatches 0; Indels 0, Gaps 0;		Db 241 GGCCTTTTCCTCTACCAGGGCCTCGGAAGGGATCTCCCCCCGAGTTGGCT 300 Qy 301 CCCACCTTGGACACACTGCAGCTCGCCGACTTTGCCACCACTTGGCAGCAG 360 Db 301 CCCACCTTGGACACACTGCAGCTCGCCGACTTTGCCACCACTTTGGCAGCAG 360 Qy 361 ATGGAAGAACTGGCAGCTCCTGCAGCCCACCCAGGGTGCCATTTGGCAGCAG 360 Qy 421 GCCTCTGGTTTCCAGCGCCGGGAGGGGCCCTCCATTGCCAGGCTTT 420 Qy 421 GCCTCTGGTTTCCAGCGCGGGAGGGGTCCTAGTTGCCTCCATTGCCAGGCTTT 480 Qy 421 GCTCTGGTTTCCAGCGCGGGAGGGGTCCTAGTTGCCTCCATTGCAGGGTTT 480 Qy 481 CTGGAGGTGTCGTACCGGCAGGAGGGGTCCTAGTTGCCTCCATTTGCAGAGGTTTC 480 Qy 481 CTGGAGGTGTCGTACCGGCAGGAGGGGTCCTAGTTGCCTCCATTTGCAGAGGTTTC 480 Qy 481 CTGGAGGTGTCGTACCGCCAGCCACCTTGCCCAGCCTTCCCATTTGCAGAGGTTTC 480 Qy 481 CTGGAGGTGTCGTACCGCCACCTTGCCCAGCCTT 523
Qy 241 GGCCTTTTCCTCTACCAGGGGCTCCTGGAAGGGATCTCCCCCGAGTTGGGT 300 Db 241 GGCCTTTTCCTCTACCAGGGCCTCGAGGGATCTCCCCCGAGTTGGGT 300 Qy 301 CCCACCTTGGAACACACTGCAGCTCGAGCTTGGCAGCTACTGGCAGCAG 360 Db 301 CCCACCTTGGAACACACTGCAGCTGGCAGCTTTGCCACCACCATCTGGCAGCAG 360 Qy 361 ATGGAAGAACACACTGCAGCTGGACGCCGACCTTTGCCACCACCATCTGGCAGCAG 360 Qy 361 ATGGAAGAATGGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCTTC 420 Qy 421 GCCTCTGCTTTCCAGCGCCGCGCAGCAGGAGGCCCACCCA	PAT 10-A	Yamasaki, M., Yokoo, Y., Yamaguchi, Polypeptide derivatives of human factor Patent: US 5714581-A 1 03-FEB-199 Location/Qualifiers 1. 525 /organism="unknown" /mol_type="unassigned DB	Query Match Best Local Similarity 100.0%; Pred. No. 2.56-86; Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY 1 ACCCCCTGGGCCCTGCCAGCTCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAGCAA 60 Db 1 ACCCCCTGGGCCCTGCCAGCTCCTGCCCCAGAGCTTCTTGCTCAAGTGCTTAGAGCAA 60 OY 61 GTGAGGAAGATCCAGGCGATGGCGCAGGGCTCCAGGAGAGCTGTGCACCTACAAG 120 OY 61 GTGAGGAAGATCCAGGCGATGGCGCAGGGCTCCAGGAGAAGCTGTGCACCTACAAG 120	CTGTGCCCCCGAGGAGCTGCTGCTGCCCCCGAGCATCCCCCGGGCTCCCCCGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCCGGGGCTCCCCGGGGCTGCT

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HSGCSFR1 1498 bp mRNA linear PRI 21-MAR-1995
Human mRNA for granulocyte colony-stimulating factor (G-CSF)
(pBRV-2).
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1 (bases 1 to 1498)
Nagata,S., Tauchiya,M., Asano,S., Yamamoto,O., Hirata,Y.,
Kubota,N., Oheda,M., Nomura,H. and Yamazaki,T.
The chromcsomal gene structure and two mRNAs for human granulocyte colony-stimulating factor
BMBO J. 5 (3), 575-581 (1986)
                                                  GCCTCTGCTTTCCAGCGCCGGGCAGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTC 480
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                                                                                                          553 GCCTCTGCTTTCCAGCGCCGCCAGGGGGTCCTAGTTGCCTCCCATCTGCAGAGCTTC
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100.0%; Pred. No. 2.1e-86;
iive 0; Mismatches 0;
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1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Data kindly reviewed (19-JUN-1986) by Location/Qualifiers
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
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colony stimulating fac
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                           Eukaryotta.

Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 660)

Devlin, J.J., Devlin, P.E., Myambo, K., Lilly, M.B., Rado, T.A. and

Warren, M.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACCCCCTGGGCCCTGCCAGCTCCTTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAGCAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression of granulocyte colony-stimulating factor by human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43. .132
/note="granulocyte colony stimulating factor signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Original source text: Human MIA PaCa-2 cell line, cDNA to (library of Kawasaki et al.), clone pP12.

Location/Qualifiers
1. 660

    .654
    'product="granulocyte colony-stimulating factor"

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100.0%; Pred. No. 2.4e-86;
ive 0; Mismatches 0; Indels
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87196936
3494801
                                                                                                                                                                                           stimulating factor.
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                                                                                             Human granulocyte colony M17706
                                                                                                                                                         M17706.1 GI:183040
granulocyte colony sti
Homo sapiens (human)
Homo sapiens
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1521)
Yamazaki,T., Yamamoto,O., Hirata,Y., Sekimori,Y. and Osada,J.
NOVEL POLYPEPTIDE
CTGAGCAGCTGCCCAGCCCAGCCCTGCAGCTGGCAGGCTGAGCCAACTCCATAGC
                                                                                             CCCACCTTGGACACACTGCAGCTGGACGTCGCCGACTTTGCCACCACCATCTGGCAGCAG
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                                                                      361 GGCCTTTTCCTCTACCAGGGCTCCTGCAGGCCCTGGAAGGGATCTCCCCCGAGTTGGGT
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YAMAZAKI TATSUMI, YAMAMOTO OSAMI, HIRATA YUICHI, PI
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strandedness: Double;
topology: Linear;
hyporhetical: No;
anti-sense: No;
c *source: cell_type=oral cavity tumor cells;
c *source: cell_line=CHU-2;
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/note='human G-CSF prewsor'
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/note='human G-CSF'
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/organism="Homo sapiens"
/mol_type="genomic RNA"
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JP 1987129298-A/1.
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Devlin, J.J., Devlin, P.E., Kawasaki, E.S. and Warren, M.K.
Expression of g-csf and muteins thereof and their use
Patent: RP 025643-A1 11 24-FEB-1988;
Location/Qualifiers
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100.0%; Score 523; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.1e-86;
Matches 523; Conservative 0; Mismatches 0;
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Job time: 2729.62 secs
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                       CTGTGCCACCCCGAGGAGCTGGTGCTGCTCGGACACTCTCTGGGCATCCCCTGGGCCTCCC
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                                                             CTGAGCAGCTGCCCCAGCCCAGGCCCTGCAGCTGGCAGGCTTGAGCCAACTCCATAGC
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Devlin,J.J., Kawasaki,E.S. and Warren,M.K.
Patent: WO 8801297-A 1 25-FEB-1988;
Location/Qualifiers
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100.0%; Score 523; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.1e-86;
Matches 523; Conservative 0; Mismatches 0;
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BX55506 BX56506
                                                                                                                                                                                                                                                                                                                                                                                                                   346 bp mRNA linear EST 10-APR-2003 trcx1 (10261) Rattus norvegicus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
Rattus norvegicus (Abrattus norvegicus)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA 91320-1799,
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Amgen EST Program.

Amgen EST Program.

Unpublished (2003)

Contact: Dan Fitzpatrick

Amgen, Inc

One Amgen Center Drive, Thousand Oaks, CA

Tel: 805 447-4881

Plate: 00003 row: c column: 7.

Location/Qualifiers

1. 346

/organism="Rattus norvegicus"
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trcx1-00003-c7 5', mRNA sequence.
CB705562
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AY414901
CD013926
AY414900
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BM009358
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BM423896
BM915836
BM556479
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BM554035
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BI960812
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CNS02GVH
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CC100458
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CB136760 K-EST0189
CB126975 K-EST0176
CB127794 K-EST0177
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Result No.

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/ Lissue type="Uterine"
/ cell type="Spithelial"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Bukaryota, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 554)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                                                                                                                                                                                                           118 AGGAÁGCCACCÓCCTGGCCTGCCAGGCTCCCTGCCCAGAGCTTCCTGCTCAAGTGCT 177
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
S2 Eceun-dong Yuscong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-44709
Fax: +82-42-860-4409
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                                                               Length 314;
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                                                           Score 49; DB 14; Lu
Pred. No. 0.00028;
0; Mismatches 10;
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Plate: 14 row: A column: 07
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                                                                   Query Match
Best Local Similarity 84.6%;
Matches 55; Conservative
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1 (bases 1 to 314)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHIJ6760 314 bp mRNA linear EST 29-JAN-2003
K-EST0189338 L5HLK1 Homo saplens cDNA clone L5HLK1-42-H10 5', mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="trox1-00003-c7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 GCCCGGGACTCCATGACCCAGTCTAGAACCCCCTGGGCCCTGCAGCTCCC
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tael: +82-42-860-44409
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                   Length 346;
                                                                                                                                                                                                                                                                       Query Match 28.9%; Score 52; DB 14; Length 34 Best Local Similarity 72.8%; Pred. No. 3.4e-05; Matches 67; Conservative 0; Mismatches 25; Indels
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CB136760
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BG548320 598 bp mRNA linear EST 04-APR-2001 602575289F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703159 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY414901 GOB bp DNA linear GSS 17-DEC-2003 Pan troglodytes CSF3 gene, VIRTUAL TRANSCRIPT, partial sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AGGAAGCCACCCCCGGGCCCTGCCAGACTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Context: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
Tissue Progration: CLONTECH Laboratories, Inc.
Thus Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1541 row: b column: 24
High quality sequence stop: 597.
High quality sequence stop: 597.

I. 598
                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1. (bases 1 to 598)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
116 AGGGAAGGACTCCGTTAGGTCCAGCCACCTGCCCCAGAGCTTCCTGCTCAAGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 598;
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llarity 84.6%; Pred. No. 0.00035;
Conservative 0; Mismatches 10;
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Homo sapiens
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1 (bases 1 to 579)

1 (bases 1 to 579)

2 (Rim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center
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K-EST0177131 CISNU17 Homo sapiens CDNA clone CISNU17-10-C09 5',
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                                                           116 AGGGAAGGACTCCGTTAGGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCT 175
                                                                                         121 AddaAgccacccccadcccradcccraccccraccccagagcrrcracracraagccr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Korea Research Institute of Bioscience & Biotechnology 52 Beoun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-866-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.2%; Score 49; DB 14; Length 579; larity 84.6%; Pred. No. 0.00035; Conservative 0; Mismatches 10; Indels
                          Indels
       Pred. No. 0.00034;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: yongsung@mail.kribb.re.kr
Plate: 10 row: C column: 09
High quality sequence stop: 579.
Location/Qualifiers
1 . 579
//mol_type="mRNA"
//mol_type="mRNA"
//db_xref="taxon:9606"
//db xref="taxon:9606"
//dloca="CISNU17-10-C09"
                                                                                                                                                                                                                                                                                                                   CB127794
CB127794.1 GI:28090473
           84.68;
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           Best Local Similarity 84.6
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                    nRNA sequence.
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Best Local Similarity
Matches 55; Conserv
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FEATURES

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

LOCUS ACCESSION

RESULT 4 CB127794

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Homo sapiens CSF3 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 634)
Clark.A.G., Glanowski, S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Reriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                             /mol_type="mana" orpromed to the property of the property of the property of the property of the property of the property of the product were subcloned into purive Cloning trame. PCR products were subcloned into purive Cloning frame. PCR products were subcloned into purive Cloning Vector and sequenced completely using M13 forward and reverse primers. Sequencing gaps were closed by re-sequencing using primers flanking the gapped areas."
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                        116 AGGGAAGGACTCCGTTAGGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                91 AGGAAGCCACCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Best Local Similarity 84.6%; Pred. No. 0.00036;
Matches 55; Conservative 0; Mismatches 10; Indels
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llarity 84.6%; Pred. No. 0.00036;
Conservative 0; Mismatches 10;
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14671302
                                               organism="Homo sapiens"
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    Location/Qualifiers
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Matches 55; Conserv
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Jin, P., Fu,G.K., Wilson,A.D., Yang,J., Chien,D., Hawkins,P.R., Au-Young,J. and Stuve,L.L.
PCR isolation and cloning of novel splice variant mRNAs from known
                                                                                Pan troglodytes (chimpanzee)
Pan troglodytes
Bukaryotus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 608)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Ford, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                            Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Glark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.U., Sninsky, J.U., Adams, M.D. and Cargill, M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Pred. No. 0.00035;
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3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pjin@incyte.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.00035;
0; Mismatches 10
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/organism="Pan troglodytes"
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Science 302 (5652), 1960-1963 (2003)
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/gene="CSF3"
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genomic survey sequence.
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AY414901.1 GI:39770860
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1 Similarity 84.6%;
55; Conservative (
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Unpublished (2003)
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Matches 55; Conserv
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                     ACCESSION
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/Glone="Wappel"
/note="Vector: pGWV-SPORT6; Site_1: ECORV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold.
Kristl A. Egland, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins.
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603629823F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5443757 5',
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Bukaryotzi.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 817)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapba-r@mail.nih.gov

Eissue Procurement: Kristi A. Egland, Ira Pastan

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bisocience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.llnl.gov

Plate: LLAM14284 row: j column: 15

High quality sequence stop: 249.
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0
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/db_xrefe"taxon:9666"
/clone="INAAGR:6722223"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
/lab_host="EMDH108"
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Pred. No. 0.00039;
0; Mismatches 10;
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/organism="Homo sapiens"
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ilarity 84.6%;
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Best Local Similarity
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90138939 Single gene library Homo sapiens cDNA, mRNA sequence.
CD013925
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1 (bases 1 to 79.

Jin, P., Fu,G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R., Au-Young, J. and Stuve, L.L.

For isolation and cloning of novel splice variant mRNAs from known thoublished (2003)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(Dases 1 to 802)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 0.00039;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Jin, P.
Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
7Tel: 650 621 8639
Fax: 650 621 8965
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1. 789
/organism="Homo sapiens"
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ISM Meno sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 906)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Numblished (1999)

A Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbar Femailiningov

Tissue Procurement: Kristi A. Egland, Ira Pastan

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14276 row: column: 15

High quality sequence stop: 712.
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267 AGGAAGCCACCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCT
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/mol Lype="mkNype""|kmy |
/mol Lype="mkNype"|kmy |
/clone="INAGE:6719127"
/cell line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
/lab_lost="EMDH10B"
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Best Local Similarity 84.6%; Pred. No. 0.00041;
Matches 55; Conservative 0; Mismatches 10; Indels
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Lupublished (2003)

Contact. Jin, P.

Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8965

Email: pjin@incyte.com;

Smail: pjin@incyte.com;

Corganism="Homo sapiens"

Anol_type="mRNA"

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ECORI; cDNA made by oligo-dT priming. Directionally cIoned
into EcoRI/Anol sites using the following 5' adaptor:
GGACGAGIG; Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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PCR isolation and cloning of novel splice variant mRNAs from known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AGGGAAGGACTCCGTTAGGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCT 175
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 897)
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Pred. No. 0.00039;
0; Mismatches 10; Indels
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Best Local Similarity 84.6%;
Matches 55; Conservative (
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Best Local Similarity
Matches 55; Conserv
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SOURCE

KEYWORDS

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

ORIGIN

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Search completed: October
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NITH_MGC_115"
/clone_lib="NITH_MGC_115"
/clone="Organ: pooled brain, lung, testis; Vector:
/clone_Torgan: pooled brain, lung, testis; Vector:
/clone_Corgan: pool of 6 male brains, age range 23-27; lund = brains, age range 23-27; lund = brains, age range 23-27; lund = brains, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code
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                                                                                                                                                In (bases 1 to 948)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLONA Library Arrayed by: The I.M. AG.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

Plate: LLAM11441 row: k column: 02

High quality Sequence stop: 845.
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                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Pred. No. 0.00042;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                  Homo sapiens (human)
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Tissue Procurement: DCTD/DTP

CONNA Library Preparation Rubin Laboratory

CONNA Library Preparation Rubin Laboratory

CONNA Library Preparation Fibe 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: WGC clone distribution infermation can be

Redund through the 1.M.A.G.E. Consortium/LLNL at:

http://Amage.llnl.gov

High quality sequence stop: 593.

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Publication No. US20030153049A1

GENERAL INFORMATION:
APPLICANT: LEE, SANG-YUP

APPLICANT: LEE, SANG-YUP

APPLICANT: LEE, SECHERICHIA COLI STRAIN SECRETING HUMAN

TITLE OF INVENTION: BEAULUCYTE COLONY STIMULATING FACTOR (G-CSF)

FILE REFERENCE: HYLEE60.001APC

CURRENT APPLICATION NUMBER: US/10/009,792A

CURRENT PILING DATE: 2000-10-29

PRIOR APPLICATION NUMBER: PCT/KR01/00549

PRIOR PILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PESESEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 180
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100.0%; Pred. No. 1.2e-53;
iive 0; Mismatches 0;
US-10-083-446-73
US-110-083-446-77
US-110-083-446-74
US-110-083-446-74
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    Similarity 100.
    TYPE: DNA
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2: /cgr2_6/ptodata/2/pubpna/PCT_REW PUB.seq:*

3: /cgr2_6/ptodata/2/pubpna/PCT_REW PUB.seq:*

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19: /cgr2_6/ptodata/2/pubpna/US60_NEW PUB.seq:*
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Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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Thomas, John W. TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
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; OTHER INFORMATION: B. subtilis xylanase sequence with added restriction site
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                                                                                                                                                                                                               64 TIGITITICGGCAACCGCCTCTGCAGCTAGCACAGACTACTGGCAAATTGGACTGATGG 122
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CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
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  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Abrams, Mark A.
APPLICANT: Abrams, S. C.
Bauerr, S. C.
Braford-Goldberg, Sc
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kuman
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; Sequence 11, Application US/10237386

; Publication No. US20030180895A1

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ORGANISM: Unknown
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                                                                                                                                                                            Sequence 24, Application US/10009792A
; Publication No. US20030153049A1
; Publication No. US20030153049A1
; Publication No. US20030153049A1
; Publication No. US20030153049A1
; Publication No. US20030153049A1
; APPLICANT: JEDGNG, Ki-Uun
; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
; TITLE PEPERENCE: HYLESGO, 001APC
; CURRENT APPLICATION NUMBER: US/10/009,792A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: RR 10-200-0017052
; PRIOR APPLICATION NUMBER: RR 10-2000-0017052
; PRIOR APPLICATION NUMBER: RR 10-2000-0017052
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AGGACTCCGTTAGGTCCAGCCAGCTCCTGCCCAGAGCTTCCTGCTCAAGTGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCAGAGCTTCCTGCTCAGTGC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86; DB 15; Le
Pred. No. 3.1e-20;
0; Mismatches 0;
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Pred. No.
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79.0%;
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Best Local Similarity 77.6%;
Matches 135; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-10-009-792A-24
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Best Local Similarity
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US-10-009-792A-24
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Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
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Correstopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 546;
                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CRASSIFICATION: «Unknown»
PRIOR APPLICATION AUNBER: 08/762,227
FILING DATE: 08-DEC-1996
FILING DATE: 08-DEC-1996
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 16-FUN-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS,MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.1%; Score 50.6; DB 15; 93.0%; Pred. No. 2.4e-07; cive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCCAGAGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 178:
                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bauer, S. C.
Bradrod-Goldberg, Sc
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/10083446 Publication No. US20030185790A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas, John W. TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abrams, Mark A. Bauer, S. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 178
  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 63167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-083-446-178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ACTCCGTTAGGTCCAGCCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
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Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                           COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.1%; Score 50.6; DB 15; 93.0%; Pred. No. 2.4e-07;
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-P6-2002
CLASSIFICATION: «UDKNOWN»
PRIOR APPLICATION NUMBER: U8/192,325
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 177:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
Oolins, Peter O.
Paik, Kumnan
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Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
STREET: 800 N. Lindbergh
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (636)737-6257
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.0
Matches 53; Conservative
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STATE: Missouri
COUNTRY: USA
                      CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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US-10-083-446-178
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Thomas, John W. TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
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ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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COMPUTER TEADABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.1%; Score 50.6; DB 15; 93.0%; Pred. No. 3.1e-07; ive 0; Mismatches 4;
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION:
TELEPHONE: (536)737-6257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Baston, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-083-446-75; Sequence 75. Application US/10083446; Publication No. US20030185790A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 72: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 921 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 53; Conserv
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CORRESPONDENCE ADDRESS:
CORPORATE Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.1%; Score 50.6; DB 15; Length 906; Best Local Similarity 93.0%; Pred. No. 3e-07; Matches 53; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>
                                 PRICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
Thomas, John W.
                                                                                                                                                                                                                                                                                                          NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 72, Application US/10083446 Publication No. US20030185790A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               (636) 737-6257
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (636)737-5422
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Abrams, Mark A.
                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 63167
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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Ex-Vivo Expansion Of Hematopoietic Cells variant (IL-3) Hematopoiesis Chimera Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IDPPY disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/192,325
FILING DATE: 06-MUN-1995
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                  Query Match
28.1%; Score 50.6; DB 15
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
Matches 53; Conservative 0; Mismatches 4
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Braford-Goldberg, Sarah R.
Caparon, Maire H.
Baston, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: S. Christopher Bauer,
                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Methods Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 84, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION
                                            TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 63167
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 800 N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
INFORMATION FOR SEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,446

FILING DATE: 26 Feb-2002

CLASS:FICATION SUMBER: 08/10/27

FILING DATE: 09-DEC-1996

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14 FEB-1994

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14 FEB-1994

APPLICATION NUMBER: US 08/192,325

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.1%; Score 50.6; DB 15
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
Matches 53; Conservative 0; Mismatches 4
               ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELEPHONE: (636)737-6257
TELEPHONE: (636)737-5452
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6.
                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 75:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bauer, S. C.
Braford-Goldberg, S.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 78, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Baner, S. C.
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                            LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-083-446-78
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Thomas, John W.

IITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                     445 ACACCATTAGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 501
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF CLEAR ADDRESS:
CORRESPONDENCE ADDRESSE: S. Christopher Bauer, Pharmacia Corporation
ADDRESSEE: S. Christopher Bauer, Mail Zone O4E
Corporate Patent Dept., Mail Zone O4E
                                                                                                                     .
0
                                                                  Length 966;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYEE: Floppy disk

CONFUNTER: ISM PC compatible

CORFATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/083,446

FILING DATE: 26-Feb-2002

CLASSIFCATION: CURNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: US 08/446,872

FILING DATE: 08-DEC-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                     Indels
                                                                                                                                                                      124 ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCT
                                                                     Query Match
28.1%; Score 50.6; DB 15;
Best Local Similarity 93.0%; Pred. No. 3.1e-07;
Matches 53; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.1%; Score 50.6; DB 15; 93.0%; Pred. No. 3.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bauer, S. C.
Braford-Goldberg, Sarah R.
Gaparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
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; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-10-083-446-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corporate Paten
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                 US-10-083-446-70
Sequence 70, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: (636)737-6257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    737-5452
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (636)737-5.
INFORMATION FOR SEQ ID NO: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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Best Local Similarity
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IIILE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
                                                                                                                                                                                                                                                                                                 124 ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
                                                                                                                                                                                                                                                                                                                             400 ACACCATTAGGCCCTGCCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 456
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: G. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
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                                                                                                                                                                                                Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 26-Feb-2002
CLASSIFICATION: CURNOWn>
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                  Query Match 28.1%; Score 50.6; DB 15; Best Local Similarity 93.0%; Pred. No. 3.1e-07; Matches 53; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-083-446-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 68, Application US/10083446
Publication No. US20030188790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (636)737-6257
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Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumman
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
            LENGTH: 921 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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US-10-083-446-68
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Gaps

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4; Indels

Mismatches

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Conservative

53;

Matches

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Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ACACCATTAGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPSTATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCCAGAGCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.1%; Score 50.6; DB 15;
llarity 93.0%; Pred. No. 3.1e-07;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
PILING DATE: 06-JUN-1995
                                                                                                                                                                    Sarah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: October 9, 2004, 06:22:17
Job time : 154.651 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: S. Christopher Bauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                           Bauer, S. C.
Braford-Goldberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (636) 737-6257
                                                                                                                                                                                          Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                             McKearn, John P.
Olins, Peter O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                       Abrams, Mark A.
                                                                        US20030185790A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: St. Louis
STATE: Missouri
                                                 ; Sequence 73, Application
; Publication No. US2003018
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                       APPLICANT:
    RESULT 15
US-10-083-446-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-083-446-73
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas, John W. TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
124 ACTCCGTTAGGTCCAGCCAGCTCCCTGCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 180
                                               445 ACACCATTAGGCCCTGCCAGCTCCCTGCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACCATTAGGCCCTGCCAGCTCCCTGCCCAGAGCTTCCTGCTCAAGTGCTTAGAG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone O4E
STREET: 800 N. Lindbergh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURENT APPLICATION DATA: APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: UNMBER: US/10/083,446
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
ATTORNEY/AGENT MARGER: 42,305
ATTORNEY/AGENT MARGER: 42,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.1%; Score 50.6; DB 15; 93.0%; Pred. No. 3.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
                                                                                                                                                                                                                                                      Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Clins, Perer O.
Paik, Kumnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
                                                                                                                                                            Sequence 71, Application US/10083446 Publication No. US20030185790A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 966 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (636)737-5452 INFORMATION FOR SEQ ID NO: 71:
                                                                                                                                                                                                                               APPLICANT: Abrams, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 63167
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: St. Louis
STATE: Missouri
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                                                                                                                                        10-083-446-71
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Matches 53
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TAGAG 180

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